

NUKLEINSÄUREARRAY BESTEHEND AUS SELEKTIVEN MONOZYTEN-MAKROPHAGEN-GENE

Beschreibung

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Die Erfindung betrifft einen Array bestehend aus Oligo- oder Polynukleotidsonden, die immobilisiert auf einen festen Träger aufgebracht sind. Das Array ist dadurch charakterisiert, dass auf der Oberfläche Sequenzen einer Auswahl oder aller der in den Tabellen 1-6 genannten selektiven Monozyten-Makrophagen-Gene gebunden sind. Dieser Nukleinsäure-Array ermöglicht die Diagnose der rheumatoiden Arthritis, eine begleitende Analyse der Behandlungseffektivität und die Überwachung von Nebenwirkungen bei der anti-Tumornekrosefaktor-(TNF)-Therapie und somit die Auswahl der für den jeweiligen Patienten mit rheumatoider Arthritis am wirkungsvollsten Therapie. Die vorliegende Erfindung betrifft ferner einen Nukleinsäure-Array zur Prognose und zur Entwicklung neuer anti-TNF gerichteter Pharmaka oder solcher Pharmaka, die in dessen Regelkreis eingreifen.

Die Zellen des Monozyten / Makrophagen-Systems sind an der Aktivierung und Aufrechterhaltung von Entzündungskaskaden im Blut und im Gewebe z. B. im Rahmen der rheumatoiden Arthritis und bei anderen chronisch entzündlichen Erkrankungen, aber auch bei autoaggressiven Erkrankungen wesentlich beteiligt. Bei diesen Erkrankungen sind Monozyten und Makrophagen hoch aktiviert, zeigen Veränderungen im Besatz ihrer Oberflächen-Moleküle, treten mit anderen Zellen in Kontakt und sezernieren bestimmte Botenstoffe wie u. a. TNF-alpha, die dafür sorgen, den Entzündungsvorgang zu unterhalten. TNF-alpha ist ein von Monozyten / Makrophagen, Lymphozyten und Mastzellen gebildetes Zytokin mit Einfluss auf Entzündung, Sepsis, Lipid- und Proteinstoffwechsel, Blutbildung, Angiogenese, Wund-

heilung und Immunabwehr, das aber auch zytolytische bzw. zytostatische Wirkung auf Tumorzellen hat.

Bei entzündlichen Erkrankungen zeigen Monozyten
5 Makrophagen ein charakteristisches, pathologisch verändertes Genexpressionsmuster mit deutlichen Abweichungen im Vergleich zu gesunden Probanden. Mit dem Fachmann bekannten bioinformatischen Methoden wie z. B. der Signifikanz- und Clusteranalyse lassen sich u. a. Gene mit ähnlichem Verhalten und hoch- oder niederregulierte Gene aus
10 den Hybridisierungsmustern eines Nukleinsäurearrays bestimmen.

Die zunehmende Verfügbarkeit der Hochdurchsatz-Verfahren
15 in Form von Nukleinsäurearrays, die exponentiell anwachsenden Informationen zum humanen Genom und der Genexpression, sowie die globale Vernetzung von Datenbanken mit strukturierten biomedizinischen Informationen wird die Betrachtungsweise chronisch entzündlicher und entzündlich-rheumatischer Krankheitsbilder grundlegend verändern.
20 Aus dem verbesserten Verständnis der molekularen Grundlagen der zell-, gewebs- und krankheitsspezifischen Genexpression lassen sich die molekularen Abläufe definieren und tragen dazu bei, eine frühere Diagnose und
25 verbesserte Prognose zu erlauben. Zum anderen gewährleisten Mikroarray-Technologien effektivere Therapieformen für die rheumatoide Arthritis und für andere chronisch entzündliche Erkrankungen zu entwickeln und ermöglichen ein schnelles Screeningsystem. Ferner erlauben diese multiplen Verfahren die Entwicklung von pharmazeutischen und biologisch wirksamen Medikamenten (Biologicals) zu beschleunigen und die Testphasen der Medikamentenwirkung, wie auch die Beurteilung der Medikamenten Nebenwirkungen schneller beurteilen zu können. Aus diesem Grund stellt

dieses Verfahren einen volkswirtschaftlichen und wirtschaftlichen Gewinn dar.

Die Mikroarray Technologie stellt eine Miniaturisierung analytischer Verfahren auf der Basis der DNA- bzw. RNA-Hybridisierung im Hochdurchsatz-Verfahren dar. Gleichzeitig können dadurch viele tausend verschiedene DNA/DNA- (DNA/RNA-) Wechselwirkungen innerhalb eines Testansatzes analysiert werden. mRNA-Expressionsprofile werden mittels DNA-Arrays durch die Hybridisierung von markierten cRNA oder cDNA-Proben bestimmt. Diese Technologien erfordern ein hohes Maß an Automatisierung und Standardisierung mit Aufbau und Nutzung entsprechender Proben- und Datenbanken (Sequenzinformationen, Oligonukleotide). Die derzeit verwendeten DNA-Arrays unterscheiden sich im Trägermaterial (Nylonmembranen, Glasoberflächen, Edelmetall bedampfte Glasoberflächen, Kunststoffe), der Länge bzw. der Herstellung der an den Träger immobilisierten DNA-Sequenzen und der Markierungstechnik für eine zu bindende Probe. In Analogie zu den Methoden der DNA-Hybridisierung beim Southern-/Dot-Blot können DNA-Sequenzen auf einem Filter punktförmig und in systematischer Reihenfolge mit einem Druckkopf durch Spotting, durch Piezo-Druckverfahren (Tintenstrahltechnologie) oder durch Photolithographie (chemische Direktsynthese auf dem Trägermaterial) fixiert werden. Die DNA kann dabei eine cDNA, ein PCR-Produkt oder ein synthetisch hergestelltes Oligonukleotid sein. Jede dieser aufgetragenen Sequenzen ist damit einem spezifischen Ort in einer bekannten Anordnung zugeteilt. Aus einer klinischen oder aber pharmazeutisch zu untersuchenden Probe kann RNA aufgereinigt werden und nach Umschreibung durch reverse Transkription mit den auf dem Array befindlichen komplementären Nukleinsäurensträngen die in einer hohen genomweiten Anzahl oder aber einer bereits

vorselektionierten Anzahl aufgebracht sind hybridisiert werden. Die Markierung der Probe erfolgt dabei mittels eingebauter radioaktiver Nukleotide, über Biotin-Streptavidin Wechselwirkungen, Digoxigenin-Enzym Verstärkungen oder aber über direkte oder indirekte eingebaute Fluoreszenzfarbstoffe. Das Auslesen der Information erfolgt über die Intensität der Radioaktivität oder der Fluoreszenz an einem spezifischen Ort des Trägermaterials und lässt somit Rückschlüsse zu, welche relative Menge an spezifisch gebundener DNA- bzw. RNA-Sequenz in der markierten Probe vorhanden war.

Das An- und Abschalten von Genen ist Grundlage aller biologischen Prozesse und außerdem eine extrem sensitive Antwort auf veränderte äußere Bedingungen. Mit der Extraktion von RNA aus einer biologischen Probe, dem Einwirken von markierter cDNA oder RNA auf einen Nukleinsäure-Array (Hybridisierung) und dessen Analyse ist innerhalb kürzester Zeit eine große Fülle von Informationen über den Zustand der Zellen in der biologischen Probe unter veränderten Bedingungen möglich. Die auf der Hybridisierung von Nukleinsäuren beruhende Technologie hat den Vorteil einer extrem hohen Spezifität, Sensitivität und relativ leichten, schnellen Durchführbarkeit.

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Geschieht das An- oder Abschalten von Genen in Monozyten/Makrophagen in nicht physiologischer Weise, so kann es die Ursache von entzündlichen Erkrankungen oder ein messbares Zeichen für diese sein. Die Therapie mit anti-TNF wirksamen Medikamenten sollte im Idealfall die pathologisch veränderte Genexpression in den betroffenen Zellen auf das Niveau von gesunden Patienten normalisieren.

Durch Untersuchung der Genexpressionsprofile ist zu erwarten, dass eine neue molekulare Charakterisierung der rheumatoiden Arthritis und anderer chronisch entzündlicher Erkrankungen möglich wird und damit eine Einteilung
5 in Subgruppen nach pathophysiologischen Besonderheiten erfolgt. Bei den entzündungshemmenden anti-TNF Therapien stehen somit prognostische Vorhersagen in Aussicht über die Agressivität im weiteren Verlauf. Dies würde bereits frühzeitig Einfluß auf die Wahl und Intensität der medikamentösen Therapie mit den bisher bekannten bei chronischen Entzündungen verwendeten Medikamenten, aber auch mit biologisch wirksamen TNF-Blockern ausüben. Zum anderen ergeben sich hieraus weitere Ansatzpunkte, um die Therapieform im Hinblick auf die potentiellen Nebenwirkungen durch Einflussnahme dieser Medikamente zu gestalten und die Auswirkung der Nebenwirkungen rechtzeitig abzuschätzen.
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Durch anti-TNF gerichtete Therapien bei der rheumatoiden Arthritis und anderen chronisch entzündlichen oder auto-aggressiven Erkrankungen wird zum einen eine potentielle Entstehung neoplastischer Veränderungen bis hin zur Tumorbildung diskutiert, zum anderen vermindert die anti-TNF Therapie die Immunabwehr, sodass bei den behandelten Patienten vermehrt Infektionen auftreten, u. a. Tuberkulose.
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Mit Hilfe von Nukleinsäure-Array-Systemen kann die Expression tumorrelevanter Gene im Verlauf der anti-TNF Behandlung überprüft und somit frühzeitig Hinweise auf mögliche neoplastische Veränderungen geben, so dass einer beginnenden Tumorentwicklung rechtzeitig entgegengesteuert und die anti-TNF Therapie entsprechend angepasst oder falls nötig abgebrochen werden kann.
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Der Erfindung liegt die Aufgabe zugrunde, Mittel zur Überwachung der Wirksamkeit sowie von Nebenwirkungen der anti-TNF Therapie zu schaffen, aber auch die Feindiagnostik einer entzündlichen Erkrankung und damit die Auswahl der für den jeweiligen Patienten effektivsten Therapieform zu ermöglichen. Eine weitere Aufgabe der vorliegenden Erfindung besteht darin, die Wirksamkeit und Nebenwirkungen neuer anti-TNF gerichteter Pharmaka im Rahmen von klinischen Studien zu verfolgen. Erfindungsgemäß wird ein neuer Array geschaffen bestehend aus Oligo- oder Polynukleotidsonden, die immobilisiert auf einem festen Träger aufgebracht sind. Verglichen mit bisher bekannten genomweiten DNA-Chips ist der Vorteil der Erfindung eine Kostenersparnis bei der Herstellung des Nukleinsäurearrays, weil es überwiegend nur Gene enthält, die zur Lösung der Aufgabe der Erfindung interessant sind, was den Aufwand der Datenauswertung minimiert und damit verbilligt.

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Erfindungsgemäß wird die Aufgabe durch einen Nukleinsäure-Array gelöst, auf dessen Oberfläche Sequenzen einer Auswahl oder aller der in den Tabellen 1 bis 6 genannten selektiven Monozyten-Makrophagen-Gene aufgebracht sind. Anhand des Gen- oder Sequenznamens oder der Accession-Nummer kann die Sequenz aus öffentlich zugänglichen Datenbanken, vorzugsweise GeneBank oder EMBL, ermittelt werden. Die Sequenzen der aus dem Array befindlichen Nukleinsäuren können aus Genen bestehen, deren Expressionsniveau durch eine anti-TNF wirksame Therapie verändert wird.

Gegebenenfalls können auf dem erfindungsgemäßen Nukleinsäure-Array weitere Gene vorhanden sein, vorteilhaft sol-

che, von denen bekannt ist, dass sie in jeder Zelle exprimiert werden und zur Grundausstattung der Zelle gehören. Die Gene, die für diese Nukleinsäuren codieren, werden üblicherweise als Haushalts- oder Housekeeping-
5 Gene bezeichnet und werden zur Normierung der erhaltenen Signale verwendet. Das Array kann die genannten Sequenzen in Form von DNA, komplementärer RNA oder chemisch modifizierten Nukleinsäuren, vorzugsweise PNA (protein nucleic acid) enthalten.

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Bei den Genen oder Gensequenzen kann es sich um krankheits- und nebenwirkungsrelevante selektionierte Gene der rheumatoiden Arthritis oder anderer chronisch entzündlicher Erkrankungen handeln, vorzugsweise aus dem Monozyten/Makrophagen-Zellsystem. Gegebenenfalls können auf den Oberfläche des Arrays auch Allele, Derivate und/oder Splicingvarianten der Gen- oder Genteilsequenzen oder Oligomersequenzen vorliegen. Die Übereinstimmung der Sequenzen auf dem Array mit den entsprechenden Sequenzen in Tabelle 1-6 soll dabei mindestens 80 % in den Protein-kodierenden Abschnitten der mRNA betragen.

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Der Träger, auf den die Nukleinsäuren aufgetragen werden, kann jeder Träger sein, der normalerweise für RNA- oder DNA Arrays verwendet wird. Die Verfahren zum Auftragen und Immobilisieren der Nukleinsäuren sind Stand der Technik und dem Fachmann bekannt. Zur Kopplung der genannten Sequenzen kann der Träger mit reaktiven Gruppen, Metallverbindungen oder Legierungen beschichtet sein. Die Gene oder Gensequenzen können beispielsweise durch Spottingverfahren, Immobilisierungsverfahren oder durch in-situ Syntheseverfahren von Oligomeren oder spiegelbildlich in Form von RNA aufgebracht werden.

Das erfindungsgemäße Array kann beispielsweise zur Messung der Monozyten/Makrophagen Aktivierung oder der Entzündungsaktivität im Blut oder Zellgewebe bei entzündlichen Erkrankungen, vorzugsweise der rheumatoiden Arthritis 5 verwendet werden. Das Array kann z. B. zur Früherkennung der genannten Erkrankungen bei genetisch vorbelasteten Patienten verwendet werden, noch bevor sich klinische Symptome manifestieren. Ein weiterer Einsatzbereich ist die Feindiagnostik, vorzugsweise die Einteilung von Patienten 10 in Subgruppen, die jeweils eine unterschiedliche Therapie und unterschiedliche Medikamente benötigen. Das Array kann ferner zur Therapieüberwachung, zur Verfolgung von Nebenwirkungen, zur Erstellung einer Prognose und zur Identifizierung neuer pharmazeutischer Targets bei 15 den genannten Erkrankungen verwendet werden.

Dazu werden den zu untersuchenden Patienten Blut oder Gewebeproben entnommen, aus denen RNA mit bekannten Standardtechniken isoliert und gegebenenfalls als Gesamt-RNA 20 oder Poly A+-RNA weiterverwendet wird. Mit reverser Transkriptase kann die RNA in cDNA umgeschrieben und dabei mit einer Markierung versehen werden, z. b. einem Fluoreszenzfarbstoff, einem radioaktiven Nuklid oder einem Enzym wie alkalische Phosphatase. Daneben kann die 25 RNA direkt markiert oder unmarkiert zur Hybridisierung des Nukleinsäure-Arrays eingesetzt werden. Nach Hybridisierung des Arrays mit den Nukleinsäureproben und nachfolgenden Waschschritten kann die Bindung der Probe an die auf dem Array befindlichen Sequenzen mit jedem geeigneten 30 Verfahren analysiert werden. Im Falle einer Fluoreszenzmarkierung sind dies optische Verfahren, bei radioaktiv markierten Proben käme eine Autoradiographie zur Anwendung und bei einer Enzymmarkierung enzymatische

Nachweisverfahren, z. B. die Umsetzung eines farblosen Substrates zu einem farbigen Produkt.

Ein inverser Nachweis von festphasengebundener Total- oder mRNA mit den Sequenzen aus Tabelle 1-6 ist ebenfalls möglich. Dazu werden auf den RNA-Mikroarrays Blut- oder gewebsspezifische RNA-Moleküle von bis zu 500 Patienten gebunden. Der qualitative / quantitative Nachweis der Transkriptmenge relevanter Gene erfolgt dann mit den in Tabelle 1-6 beschriebenen selektionierten Genen, Gennabschnitten oder Oligomeren. Die RNA-Proben werden auf Kopplungsträger gespottet und setzen sich aus Total-RNA oder messenger-RNA zusammen. Die RNA dient dabei als Target für die aus DNA-Mikroarrays abgeleiteten hoch signifikant exprimierten Gene nach Tabelle 1-6, die als markierte Sonden zur Hybridisierung eingesetzt werden. Vorgeschlagen wird das Koppeln biotinylierter RNA oder messenger-RNA auf Streptavidin beschichteten Glasträgern (Slides). Nach Markierung der RNA mit Biotinderivaten, wird die RNA auf Poly-L-Lysin behandelten vorzugsweise aber auf mit Streptavidin beschichteten Glas- oder Plastikslides durch Spotting aufgebracht und getrocknet. Eine Degradation der RNA wird so verhindert. Alternativ bietet sich eine kovalente Kopplung der RNA durch Bindung an reaktive Trägermaterialien an, die vorzugsweise durch UV-Bestrahlung katalysiert wird. Zusätzlich ist eine multiple, gleichzeitige Markierung verschiedener Gene, Gennseinheiten oder Oligomere mit verschiedenen Markierungs-Spezies, z.B. Radioaktivität, Fluoreszein, Digoxigenin und enzymatischen Markierungen vorteilhaft.

Parallel unterschiedliche Markierungen der Sonden mit unterschiedlichen Fluoreszenzfarbstoffen sind möglich. Alternativ sind enzymatische oder aber radioaktive Sonden-

markierungen zu nennen. Zur Quantifizierung und Qualitätskontrolle werden markierte Haushaltsgene (alpha-, beta, gamma-Aktin, GAPDH usw.) eingesetzt. Bevorzugt wird der Nachweis hier parallel und gleichzeitig mit maximal 50 Gensonden pro Ansatz gleichzeitig durchgeführt.

Neben der Vereinfachung der biometrischen Analyse durch Kopplung von RNA Spezies an Trägermaterialien erlaubt dieses System eine schnelle Diagnostik und bietet eine komplexe für den Patienten individuell schnelle Diagnostik, Prognostik und Therapiesteuerung. Insbesondere bei pharmakologischen Entwicklungsstrategien erlaubt das System eine schnelle Durchführung mit hohem Durchsatz.

Die folgenden Beispiele und Abbildungen dienen nur zur Erläuterung und beschränken in keiner Weise den Umfang der Erfindung.

1. Isolierung von Monozyten

Im hier angewandten Verfahren wurde die Auswahl selektiver hochreiner Monozyten des peripheren Blutes benutzt, um eine Aussage 1.) zur Krankheitsspezifität, 2.) der Anwendung des Therapeutikums anti-TNF-alpha, als "Biological", 3.) im Vergleich zum Gesunden Probanden, als auch 4.) zur Bewertung von anti-TNF-alpha relevanten gendiagnostischen Möglichkeiten, zu ermöglichen. Dabei wurden die peripheren Blut-Leukozyten aus peripherem Blut durch eine Fikollgradienten-Dichtezentrifugation angereichert. Diese Fraktion, die individuell unterschiedliche Zusammensetzung aus Monozyten (5-12%), CD4+ T-Zellen (85-92 %), CD8+ T-Zellen (5-10%), NK-Zellen (2-5%), basophilen und neutrophilen Granulozyten aufweist, wurde zur Gewinnung spezifischer Monozytenfraktionen weiteren Reinigungsschritten unterzogen. Hierbei kamen sowohl Negativ-

selektionen, bei denen sämtliche andere Zellfraktionen über magnetische Beads-Antikörper Wechselwirkungen entfernt werden, als auch Positivselektionen durch CD14+ Markierung über magnetische Beads oder aber FACS Zellsortierungsverfahren zum Einsatz. Bei beiden Verfahren ergaben sich Monozyten-Zellreinheiten von ca. 96 %.

2. RNA-Gewinnung

Die reinen Monozytenfraktionen wurden in RNA-Lysepuffer aufgenommen und die RNA dann über einen kommerziell erhältlichen RNA Reinigungskit (Qiagen) gereinigt. Die RNA wurde über etablierte cDNA Umschreibemethoden durch reverse Transkription in cDNA umgeschrieben und dann einem weiteren linearen Amplifikationsschritt durch das angewandte "Eberwine Protokoll" zur Herstellung von aRNA (amplifizierte RNA) unterzogen. Die Quantität und Qualität der RNA, cDNA, und aRNA wurde jeweils durch Gelektrophorese, photometrische Bestimmung und über Messungen mit dem Bioanalyzer 2100 (Fa. Agilent) verifiziert.

3. Affymetrix Chip Hybridisierung

Für Expressionsanalysen werden im System der Firma Affymetrix spezifische direkt aus Datenbanksequenzen abgeleitete Oligonukleotide als DNA-Proben verwendet. Diese werden auf dem Array mit Targets aus fluoreszenz-markierten revers transkribierten Proben in Form von cDNA oder mit linear amplifizierten Proben in Form von aRNA hybridisiert.

Die Hybridisierung des genomweiten Affymetrix-Arrays (U-133A) und weitere Bearbeitung erfolgt maschinell unter Standardbedingungen nach Angaben des Herstellers Affymetrix in einem speziellen Hybridisierungs- und Waschgerät mit den speziellen Puffern. Genexpressionsmuster

werden nach Hybridisierung über das Verhältnis der Fluoreszenzintensitäten bei einer bestimmten Wellenlänge erstellt. Solche Hochdurchsatz-Expressionsanalysen erlauben Vergleiche der Expressionsmengen von Genen gleichzeitig 5 in gesundem und krankem Personen oder Vergleiche der Genexpression vor und nach Arzneimittelzugabe zur Risikoabschätzung (Pharma-/Toxikogenomik), zur Feindiagnostik und Abschätzung der Komplexität von Erkrankungen.

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4. Datenauswertung

Zum Einsatz kamen dabei mRNA Proben aus peripheren Blut-Monozyten 1.) gesunder Blutspender, 2.) chronisch aktiver Patienten mit rheumatoider Arthritis vor Behandlung und 15 3.) nach Behandlung mit TNF-alpha Antikörpern. Der Behandlungserfolg wurde über laborklinisch eindeutige Parameter und nach den klinisch anzuwendenden Kriterien der internationalen gültigen Parameteruntersuchungen (ACR-Kriterien) abgeschätzt. Ziel und Zweck dieser Dreigruppenuntersuchung war es, charakteristische Genexpressionen 20 in folgenden Gruppedefinitionen festzustellen:

1. Eine genregulatorische Krankheitsspezifität bei der aktiven unbehandelten rheumatoiden Arthritis, im Vergleich zur Genexpression gesunder Probanden.
2. Eine genregulatorisch spezifische Interpretation der anti-TNF-alpha-Behandlung zu charakterisieren und eine Bewertung der Behandlung im Vergleich zur Genexpression der aktiven unbehandelten Krankheit und im Vergleich zur Genexpression der gesunden Probanden durchzuführen.

3. Die Bewertung von Nebenwirkungen durch das Medikament="Biological" anti-TNF zu gewährleisten. Hierbei wurde die spezifische Genexpression der anti-TNF-alpha behandelten Patienten mit rheumatoider Arthritis mit der Genexpression der unbehandelten selben Patienten, und der von gesunden Blutspender verglichen.

Die Bearbeitung und Messung der einzelnen Genexpressionen innerhalb des genomweiten humanen Affymetrix-Arrays (U-133A) erfolgte innerhalb des zugehörigen Affymetrix Hybridisierungs-/ Wasch- und Auslesegerät - System. Die Auswertung vollzieht sich in 4 Schritten:

- 15 1. Bestimmung der bei der Expressionsanalyse detektierten signifikanten Gene, z. B. durch die „Fold-Change Method“ oder SAM („Significance Analysis of Microarrays“).
- 20 2. Separation der signifikanten Gene in verschiedene Sub-Populationen auf der Grundlage der Untersuchung der Expressionseigenschaften dieser Gene mittels Cluster-Analyse mit Verfahren wie „Hierarchical Clustering“, „Self-Organizing Maps“ oder „k-Means-Clustering“.
- 25 3. Auswertung des Verhaltens der signifikanten Gene innerhalb der Cluster unter Einbeziehung der klinischen Informationen (rheumatoide Arthritis (RA), anti-TNF-Therapie) und nach den Erfahrungswerten von Spezialisten.

4. Zuordnung der beteiligten Gene nach biologischen Pathways.

Allgemeines Verhalten der signifikanten Gene innerhalb der Cluster:

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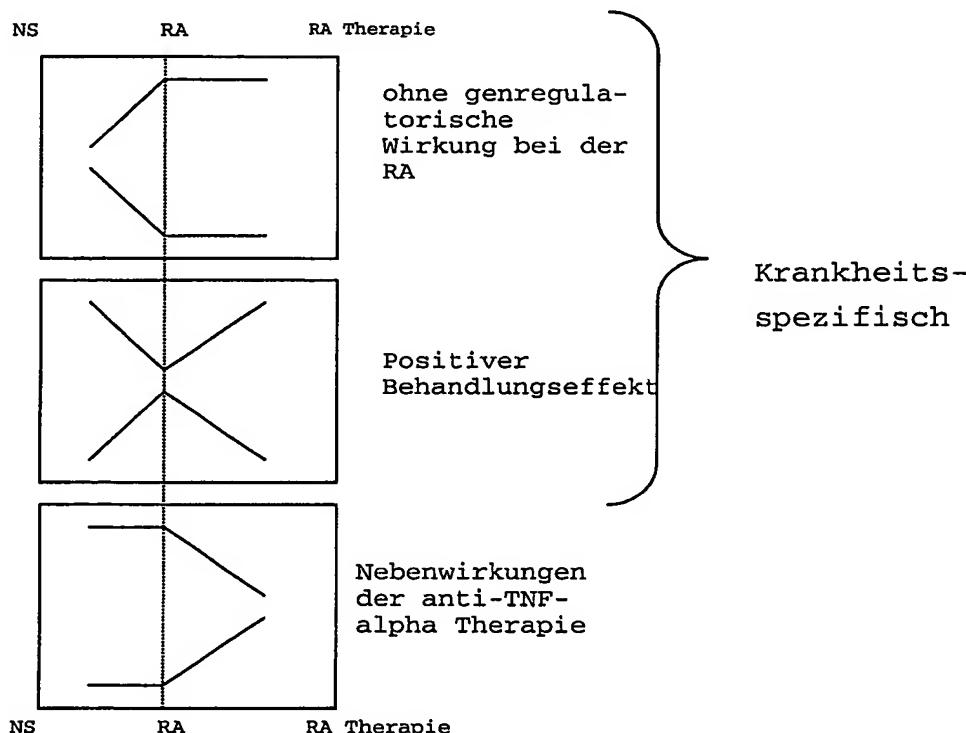


Abb. 1: schematische Darstellung der Clusteranalyse

- 10 Das Genexpressionsverhalten eines gesunden Normalspenders (NS) sowie und eines aktiven Patienten mit rheumatoider Arthritis (RA) vor und nach einer anti-TNF-alpha Therapie wurden mittels Clusteranalyse verglichen. Die Ergebnisse sind in den Abbildungen 1 und 2 dargestellt.

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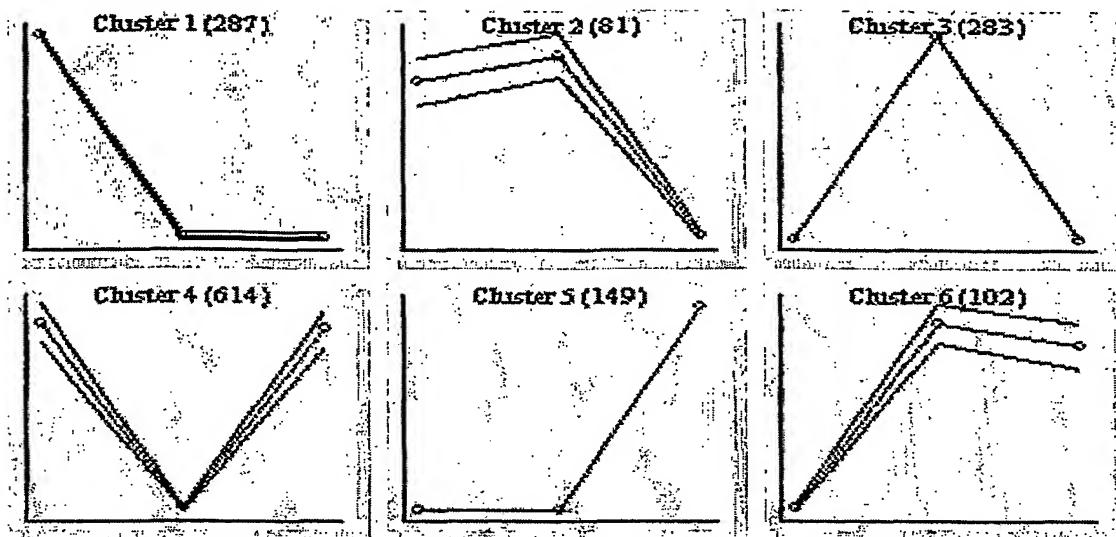


Abb. 2: Clusteranalyse anhand realer Daten.

Dargestellt sind die Genexpressionen der Clusteranalyse (n=6 Cluster). Die Anzahl der beteiligten Gene ist in Klammer wiedergegeben. Als Ergebnis der Clusteranalyse erhält man zusätzlich zum durchschnittlichen Genexpressions-Verhalten aller in einem Cluster befindlichen Gene ein Vertrauensintervall.

Die Cluster weisen dabei folgende Charakteristiken auf:

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CLUSTER-1: Die krankheitsspezifische Genexpression ist kleiner im Vergleich zum Gesunden, die anti-TNF-Behandlung ist hier ohne genregulatorische Wirkung.

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CLUSTER-2: Nebenwirkungen: Dargestellt durch die Medikamentenwirkung der Anti-TNF-alpha Behandlung besteht eine verminderte Expression der zugehörigen Gene beim behandelten Patienten.

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CLUSTER-3: Die krankheitsspezifische Genexpression größer im Vergleich zum Gesunden. Die anti-TNF-alpha Behandlung zeigt einen positiven Effekt.

CLUSTER-4: Die krankheitsspezifische Genexpression ist kleiner im Vergleich zum Gesunden. Die anti-TNF-Behandlung zeigt einen positiven Effekt.

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CLUSTER-5: Nebenwirkungen: Dargestellt durch die Medikamentenwirkung der anti-TNF-alpha Behandlung besteht eine erhöhte Expression der zugehörigen Gene beim behandelten Patienten.

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CLUSTER-6: Die krankheitsspezifische Genexpression ist größer im Vergleich zum Gesunden. Die anti-TNF-alpha Behandlung ist hier ohne genregulatorische Wirkung.

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In den Tabellen 1-6 sind die in den oben beschrieben Clustern enthaltenen Gene zusammen mit der Affymetrix Bezeichnung (links) und ihrer definierten GeneBank-Accession Nummer inkl. einer Beschreibung aufgeführt.

Tabelle 1: Gene aus Clusteranalyse 1

Affymetrix- interne Be- zeichnung	Beschreibung der Sequenz in der GeneBank Datenbank
211654_x_at	gb:MI:7565_1 /DEF=Human MHC class II DQ-beta associated with DR6, DQ1 protein, complete cds. /FEA=mRNA /GEN=HLA-DQB1 /DB_XREF=gi:188188 /FL=gb:MI:7565_1
213831_at	Consensus includes gb:X00452_1 /DEF=Human mRNA for DC classII histocompatibility antigen alpha-chain. /FEA=mRNA /PROD=DC classII histocompatibility antigen alpha-chain /DB_XREF=gi:32265 /UG=Hs.198253 major histocompatibility complex, class II, DQ alpha 1
212203_x_at	Consensus includes gb:BF338947 /FEA=EST /DB_XREF=gi:11285367 /DB_XREF=est:602036012F1 /CLONE=IMAGE:4184090 /UG=Hs.182241 interferon induced transmembrane protein 3 (1-80)
209480_at	gb:MA:6276_1 /DEF=Human MHC class II HLA-DR2-Dw12 mRNA DQ1-beta, complete cds. /FEA=mRNA /GEN=HLA-DRB2 /DB_XREF=gi:188397 /UG=Hs.73931 major histocompatibility complex, class II, DQ beta 1 /FL=gb:MG0028_1 qb:MI:7564_1 qb:NM:1140_1 qb:NM:1111_1 qb:MI:6216_1 qb:NM:002123_1
218345_at	gb:NM:018487_1 /DEF=Homo sapiens hepatocellular carcinoma-associated antigen 112 /DB_XREF=gi:8923717 /UG=Hs.12126 hepatocellular carcinoma-associated antigen 112 /FL=gb:AF288340_1 qb:NM:018487_1
221491_x_at	Consensus includes gb:AK80705_1 /FEA=EST /DB_XREF=gi:12876632 /DB_XREF=est:oc35312_81 /CLONE=IMAGE:1351702 /UG=Hs.219930 major histocompatibility complex, class II, DR beta 3 /FL=gb:NM:022555_1 qb:NM:022555_1 qb:NM:026038_1 qb:NM:09599_1 qb:NM:195819_1 qb:NM:68325_1
211734_s_at	gb:BG00512_1 /DEF=Homo sapiens, Fc fragment of IgE, high affinity I, receptor for, alpha polypeptide, clone NCC:14507, mRNA, complete cds. /FEA=mRNA /PROD=Fc fragment of IgE, high affinity I, receptor for, alpha polypeptide /DB_XREF=gi:13543505 /FL=gb:BG005912_1
201330_at	gb:NM:002887_1 /DEF=Homo sapiens arginyl-tRNA synthetase (ARS), mRNA, /FEA=mRNA /GEN=RARS /PROD=arginyl-tRNA synthetase /DB_XREF=gi:1506128 /UG=Hs..180832 arginyl-tRNA synthetase (ARS), mRNA, /FEA=mRNA /GEN=RARS /PROD=arginyl-tRNA synthetase /
201114_x_at	gb:NM:002792_1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSM7), mRNA, /FEA=mRNA /GEN=PSM7 /PROD=proteasome (prosome, macropain) subunit, alpha type, 7 /DB_XREF=gi:156188 /UG=Hs.233952 proteasome (prosome, macropain) subunit, alpha type, 7 /FL=gb:BC004427_1 qb:AB022815_1 qb:AF054185_1 qb:NM:002792_1
213418_at	Consensus includes gb:NM:0021155_1 /DEF=Homo sapiens heat shock 70kD protein 6 (HSP70B) (HSP70B), mRNA, /FEA=CDS /GEN=HSP70B /PROD=heat shock 70kD protein 6 (HSP70B) /DB_XREF=gi:14504514 /UG=Hs.3268 heat shock 70kD protein 6 (HSP70B) /EL=gb:NM:0021155_1
208951_s_at	gb:AB017493_1 /DEF=Homo sapiens mRNA for DNA-binding zinc finger (GBF), complete cds. /FEA=mRNA /PROD=DNA-binding zinc finger (GBF), mRNA, /FEA=mRNA /GEN=GBF /FL=gb:BC000311_1
217753_s_at	gb:NM:001029_1 /DEF=Homo sapiens ribosomal protein S26 (RPS26), mRNA, /FEA=mRNA /GEN=RPS26 /PROD=ribosomal protein S26 /DB_XREF=gi:1506708 /UG=Hs.299465 ribosomal protein S26 /FL=gb:BC002604_1 qb:NM:001029_1 qb:NM:001300_2
201403_s_at	gb:NM:004528_1 /DEF=Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA, /FEA=mRNA /GEN=MGST3 /PROD=microsomal glutathione S-transferase 3 /DB_XREF=gi:41758713 /UG=Hs.111811 microsomal glutathione S-transferase 3 /FL=gb:BC000505_1 qb:BC003034_1 qb:AF026971_1 qb:NM:004528_1
203103_s_at	gb:NM:014502_1 /DEF=Homo sapiens nuclear matrix protein NMP200 related to splicing factor PRP19 (NMP200), mRNA, /FEA=mRNA /GEN=NMP200 /PROD=nuclear matrix protein NMP200 related to splicing factor PRP19 /DB_XREF=gi:17657380 /UG=Hs.173980 nuclear matrix protein NMP200 related to splicing factor PRP19 /EL=gb:NM:014502_1
221903_s_at	Consensus includes gb:BE046443 /FEA=EST /DB_XREF=gi:8363496 /DB_XREF=est:hn47d10_x2 /CLONE=IMAGE:3026803 /UG=Hs.188277 KIAA0849 protein

217379_at	Consensus includes gb:AL121934 /DEF=Human DNA sequence from clone RP11-209A2 on chromosome 6. Contains an RPL10 (60S ribosomal protein L10) pseudogene, ESTs, STSS and GSSs /FEA=mRNA /DB_XREF=gi:9795199 /UG=Hs_212340 Human DNA sequence from clone RP11-209A2 on chromosome 6. Contains an RPL10 (60S ribosomal protein L10) pseudogene, ESTs, STSS and GSSs
206120_at	gb:NM_001772.1 /DEF=Homo sapiens CD33 antigen (gp67) (CD33), mRNA. /FEA=mRNA /GEN=CD33 /PROD=CD33 antigen (gp67) /DB_XREF=gi:4502654 /UG=Hs_03731 CD33 antigen (gp67) /EL=gb:NM2197.1 qb:NM_001772.1
202737_s_at	gb:NM_012321.1 /DEF=Homo sapiens U6 snRNA-associated Sm-like protein (LSM4), mRNA. /FEA=mRNA /GEN=LSM4 /PROD=U6 snRNA-associated Sm-like protein (LSM4), mRNA. /FEA=mRNA /GEN=BC003652.1 qb:AF182290.1
201416_at	gb:AF117235.1 qb:NM_012321.1 qb:AF251218.1
214044_x_at	Consensus includes gb:BG528420 /FER=EST /DB_XREF=est:60279853F1 /CLONE=IMAGE:4719060 /UG=Hs_83484 SRY (sex determining region Y-box 4 /FL=qb:NN_003107.1
204661_s_at	Consensus includes gb:AW072388 /FER=EST /DB_XREF=est:xa0705.x1 /CLONE=IMAGE:2567625 /UG=Hs_1583 neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal) 1
221666_s_at	gb:BC004470.1 /DEF=Homo sapiens baculoviral IAP repeat-containing 1 (BIRC1), mRNA. /FEA=mRNA /GEN=BIRC1 /PROD=baculoviral IAP repeat-containing 1 /DB_XREF=gi:4758751 /UG=Hs_79019 baculoviral IAP repeat-containing 1 /FL=qb:NN_004536.1
218421_at	gb:NM_0022766.1 /DEF=Homo sapiens hypothetical protein FLJ23239 (FLJ23239), mRNA. /FEA=mRNA /GEN=FLJ23239 /PROD=hypothetical protein FLJ23239 /DB_XREF=gi:12232440 /UG=Hs_34516 hypothetical protein FLJ23239 /FL=qb:NN_022766.1 qb:BC004278.1
217794_at	gb:NM_018457.1 /DEF=Homo sapiens DKFZp644J157, mRNA. /FEA=mRNA /GEN=DKFZp644J157 /PROD=DKFZp644J157 protein /DB_XREF=gi:63042 DKFZp644J157 protein /FL=qb:AR217517.1 qb:NM_018457.1
201558_at	gb:NM_003610.1 /DEF=Homo sapiens export 1, S.pombe homolog (RAE1), mRNA. /FEA=mRNA /GEN=Rae1 /PROD=Rae1 (RNA export 1, S.pombe) homolog (RAE1), mRNA. /FEA=mRNA /GEN=Rae1 /FL=qb:AB01720.1 qb:NM_003610.1
218055_s_at	gb:NM_018258.1 /DEF=Homo sapiens hypothetical protein FLJ10904 (FLJ10904), mRNA. /FEA=mRNA /GEN=BRE /PROD=hypothetical protein FLJ10904 /DB_XREF=gi:8922759 /UG=Hs_16470 hypothetical protein /FL=qb:NM_018258.1
202191_s_at	Consensus includes gb:BE439987 /FER=EST /DB_XREF=est:HTM1-745F /UG=Hs_226133 growth arrest-specific 7 /EL=qb:AB017854.1 qb:NM_005690.1.
205550_s_at	gb:NM_004899.1 /DEF=Homo sapiens brain and reproductive organ-expressed (TINFESFLA modulator) (BRE), mRNA. /FEA=mRNA /GEN=BRE /PROD=brain and reproductive organ-expressed (TINFESFLA modulator) /FL=qb:XREF=gi:475871 /UG=Hs_80426 brain and reproductive organ-expressed (TINFESFLA modulator) /FL=qb:BC001251.1 qb:NM_004899.1 qb:L38616.1
202941_at	gb:NM_021074.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2 (ubiquinone) flavoprotein 2 (24kD) /DB_XREF=gi:103035024 /UG=Hs_51299 NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) /PROD=NDUFV2 /DB_XREF=gi:103035024 /UG=Hs_51299 NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD) /EL=qb:NM_021074.1 qb:BC001632.1 qb:M2538.1
217814_at	gb:NM_020198.1 /DEF=Homo sapiens GKO001 protein (GKO001), mRNA. /FEA=mRNA /GEN=GKO001 /PROD=GKO001 protein /DB_XREF=gi:19910241 /UG=Hs_8207 GKO001 protein /FL=qb:AB113221.1 qb:BC001130.1 qb:AR22054.1 qb:NM_020198.1
212051_at	gb:NM_13996 Homo sapiens eukaryotic translation initiation factor 3, subunit 9 (eta, 116kDa) /DB_XREF=est:zj65b04.s1 /CLONE=zj65b04.s1 /UG=Hs_13996 Homo sapiens cDNA: FLJ23260 fsls, clone COL05804, highly similar to HSU90911 Human clone 23652 mRNA sequence
212386_at	Consensus includes gb:BF592782 /FER=EST /DB_XREF=gi:11685106 /DB_XREF=est:7194d06.x1 /CLONE=IMAGE:3142594 /UG=Hs_289068 Homo sapiens cDNA FLJ11916 fsls, clone HEMBB1000272
218571_s_at	gb:NM_014159.1 /DEF=Homo sapiens HSPC134 protein (HSPC134), mRNA. /FEA=mRNA /GEN=HSPC134 /PROD=HSPC134 protein /DB_XREF=gi:17661793 /UG=Hs_279761 HSPC134 protein /FL=qb:AB212243.1 qb:AF161483.1 qb:014169.1
203462_x_at	gb:NM_003751.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 9 (eta, 116kDa) (EIF3S9), mRNA. /FEA=mRNA /GEN=EIF3S9 /PROD=eukaryotic translation initiation factor 3, subunit 9 (eta, 116kDa) /DB_XREF=gi:4503526 /DB_XREF=gi:4758783 /UG=Hs_193313 NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) /
218642_s_at	gb:NM_024300.1 /DEF=Homo sapiens hypothetical protein MGCC2217 (MGCC2217), mRNA. /FEA=mRNA /GEN=MGCC2217 /FL=qb:BC002546.1
200024_at	gb:NM_001009.1 /DEF=Homo sapiens ribosomal protein S5 (RPS5), mRNA. /FEA=mRNA /GEN=RPS5 /PROD=ribosomal protein S5 /DB_XREF=gi:4506728 /UG=Hs_76194 ribosomal protein S5 /FL=qb:NN_001009.1 qb:014970.1
218101_s_at	gb:NM_004549.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) (NDUFC2), mRNA. /FEA=mRNA /GEN=NDUFC2 /PROD=NDUFC2 /DB_XREF=gi:4503526 /DB_XREF=gi:4758783 /UG=Hs_193313 NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) /EL=qb:AF037659.1 qb:NM_004559.1

209329_x_at	gb:BC000587.1 /DEF=Homo sapiens, clone NGC:2198, mRNA, complete cds. /FEA=mRNA /PROD=Unknown [protein for MGc:2198] /DB_XREF=gi:12653618 /UG=Hs.227132 mannose-binding lectin serine protease 1 (C4C2 activating component of Ra-reactive factor) /FL=db:BC000587.1
208454_s_at	gb:NM_016134.1 /DEF=Homo sapiens aminopeptidase (LOC51670), mRNA. /FEA=CDS /GEN=LOC51670 /PROD=aminopeptidase /DB_XREF=gi:7706386 /UG=Hs.218993 aminopeptidase /FL=gb:AF107834.1 gb:NM_016134.1
214351_x_at	Consensus includes gb:AH789278 /FEA=EST /DB_XREF=gi:2819398 /DB_XREF=est:aJ28b10.s1 /CLONE=1391611 /UG=Hs.180842 ribosomal protein L13
207075_at	gb:NM_004895.1 /DEF=Homo sapiens chromosome 1 open reading frame 7 (C10orf7), mRNA. /FEA=mRNA /GEN=C10orf7 /PROD=chromosome 1 open reading frame 7 /DB_XREF=gi:4757727 /UG=Hs.159483 chromosome 1 open reading frame 7 /FL=gb:AF054176.1 gb:NM_004895.1
201449_at	Consensus includes gb:AU567227 /FEA=EST /DB_XREF=gi:12920378 /DB_XREF=est:AU567227 /CLONE=CS0D027Y11 (3 prime) /UG=Hs.234M489 TIA1 cytosolic granule-associated RNA-binding protein /FL=gb:NM_022037.1 qb:NM_0171142.1
213770_s_at	Consensus includes gb:AH831675 /FEA=EST /DB_XREF=gi:5452346 /DB_XREF=est:w750qj3.x1 /CLONE=FIMAGE:2406292 /UG=Hs.78202 SWISHF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
201593_s_at	Consensus includes gb:AV716798 /FEA=EST /DB_XREF=gi:10813950 /DB_XREF=est:AV716798 /CLONE=dCBARb02 /UG=Hs.6375 uncharacterized hypothalamus protein H010_7FL-gb:AF220184.1 qb:NM_018471.1
208095_s_at	gb:NM_001222.1 /DEF=Homo sapiens calcium/calmodulin-dependent protein kinase (CaMKinase) II gamma (CaMKinase) II gamma /DB_XREF=gi:14502554 /FEA=mRNA /GEN=CAMK2G /PROD=calcium/calmodulin-dependent protein kinase (CaMKinase) II gamma /FL=gb:DR155.1 qb:NM_001222.1
201173_x_at	gb:NM_006600.1 /DEF=Homo sapiens nuclear distribution gene C (A.nidulans) homolog /NUDC, mRNA. /FEA=mRNA /GEN=NUDC /PROD=nuclear distribution gene C (A.nidulans) homolog /DB_XREF=gi:57299592 /UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog /FL=gb:BC002399.1 qb:NM_006600.1 qb:AB019498.1 qb:AF130736.1 qb:AF125465.1 qb:AF100760.1 qb:NM_006600.1
217839_at	gb:NM_006070.1 /DEF=Homo sapiens TRK-fused gene (TRFG), mRNA. /FEA=mRNA /GEN=TRFG /PROD=TRK-fused gene /DB_XREF=gi:5174718 /FG=Hs.250892 TRK-fused gene /FL=gb:NM_006070.1
203229_s_at	gb:NM_003993.1 /DEF=Homo sapiens CDC-11-like kinase 2 (CLK2), transcript variant phc11k2, mRNA. /FEA=mRNA /GEN=CLK2 /PROD=CDC-11 like kinase 2 isoform hc11k2 /DB_XREF=gi:4502882 /UG=Hs.73986 CDC-like kinase 2 /FL=gb:NM_003993.1 qb:L23218.1
203656_at	gb:NM_014845.1 /DEF=Homo sapiens KIRRA0274 gene product (KIRRA0274), mRNA. /FEA=mRNA /GEN=KIRRA0274 /PROD=KIRRA0274 gene product /FL=gb:DR8746.1 qb:NM_014845.1
218763_at	gb:NM_016930.1 /DEF=Homo sapiens syntaxin 18 (STX18), mRNA. /FEA=mRNA /GEN=STX18 /PROD=syntaxin 18 /DB_XREF=gi:8394375 /UG=Hs.13406 syntaxin 18 /FL=gb:AB028741.1 qb:NM_016930.1
213866_at	Consensus includes gb:AA382702 /FEA=EST /DB_XREF=gi:2035020 /DB_XREF=est:EST95939 /UG=Hs.3462 cytochrome c oxidase subunit VIIC
201214_s_at	gb:NM_002712.1 /DEF=Homo sapiens protein phosphatase 1, regulatory subunit 7 /DB_XREF=gi:4506012 /UG=Hs.36587 protein phosphatase 1, regulatory subunit 7 /FL=gb:BC000910.1 qb:NM_002712.1
216505_x_at	Consensus includes gb:AU118502 /DEF=Human DNA sequence from clone RP11-371119 on chromosome 20 Contains a novel gene, a gene similar to the gene for ribosomal protein S10, ESTs, STSs, GSSs and CpG islands /FEA=mRNA /GEN=YPS16 /UG=Hs.2841299 Human DNA sequence from clone RP11-371119 on chromosome 20 Contains a novel gene, a gene similar to the gene for ribosomal protein S10, ESTs, STSs, GSSs and CpG islands
203459_s_at	gb:NM_022575.1 /DEF=Homo sapiens vacuolar protein sorting 16 (yeast homolog) /DB_XREF=gi:12007657 /UG=Hs.302441 vacuolar protein sorting 16 (yeast homolog) /FL=gb:AF308801.1 qb:NM_022575.1
202880_s_at	gb:NM_004762.1 /DEF=Homo sapiens pleckstrin homology, Sec7 and coiledcoil domains 1 (cytohesin 1, isoform 1 /DB_XREF=gi:4758963 /UG=Hs.1050 pleckstrin homology, Sec7 and coiledcoil domains 1 (cytohesin 1) /FL=gb:NM_085169.1 qb:NM_004762.1 qb:NM_017456.1
43511_s_at	Cluster Incl. A1201594_9c09h12_x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1708487 /clone_end=3 /gb=A1201594 /gi:3154200 /ug=Hs.239333 /len=391
203519_s_at	gb:NM_015542.1 /DEF=Homo sapiens regulator of nonsense transcripts 2 /DB_XREF=gi:11693131 /UG=Hs.3862 regulator of nonsense transcripts 2 /GEN=RENT2 /PROD=regulator of nonsense transcripts 2 /DB_XREF=est:AF18574.1
206214_at	gb:NM_005084.1 /DEF=Homo sapiens phospholipase A2, group VII platelet-activating factor acetylhydrolase, plasma (PLA2G7), mRNA. /FEA=mRNA /GEN=PLA2G7 /PROD=phospholipase A2, group VII platelet-activating factor acetylhydrolase, plasma /DB_XREF=gi:4826883 /UG=Hs.93304 phospholipase A2, group VII platelet-activating factor acetylhydrolase,

plasma) / FI=gb:U24577.1 gb:NM_005084.1 gb:U20157.1	gb:AF020314.1 /DEF-Homo sapiens CMRF-35-H9 mRNA, complete cds. /FEA=mRNA /PROD=CORE-35-H9 /DB_XREF=gi:4103065 /
202013_s_at	gb:NM_001551.1 /DEF-Homo sapiens leukocyte membrane antigen / FI=gb:AF020314.1
202015_at	gb:NM_001551.1 /DEF-Homo sapiens immunoglobulin (CD79a) binding protein 1 (IGBP1), mRNA. /FEA=mRNA /GEN=IGBP1 / PROD=Immunoglobulin-binding protein 1 /DB_XREF=gi:457662 / UG=Hs_3631 immunoglobulin (CD79a) binding protein 1 / FI=gb:BC004137.1 gb:NM_001551.1
218138_at	gb:NM_018848.1 /DEF-Homo sapiens McKusick-Kaufman syndrome (MKKS), mRNA. /FEA=mRNA /GEN=MKKS /PROD=McKusick-Kaufman syndrome protein /DB_XREF=gi:9055271 / UG=Hs_46743 McKusick-Kaufman syndrome / FI=gb:AF221992.1
220864_s_at	gb:NM_015965.1 /DEF-Homo sapiens CGI-39 protein; cell death-regulatory protein GRIM19 /DB_XREF=gi:7705733 / UG=Hs_279574 CGI-39 protein; GEN= JOC51079 /PROD=CGI-39 protein; cell death-regulatory protein GRIM19 / FI=gb:AF15662.1 gb:NM_015965.1 cell death-regulatory protein GRIM19 / FI=gb:AF132973.1 gb:NM_015965.1
213335_at	Consensus includes gb:AF989567 /FEA=EST /DB_XREF=est:ws346448 /DB_XREF=est:ws34603.x1 /CLONE=IMAGE:249910 /UG=Hs_34578
212507_s_at	Consensus includes gb:AF809341 /FEA=EST /DB_XREF=gi:5395907 /DB_XREF=est:weg6c09.x1 /CLONE=IMAGE:2348944 /UG=Hs_170121
205992_s_at	gb:NM_000585.1 /DEF-Homo sapiens interleukin 15 (IL15), mRNA. /FEA=mRNA /GEN=IL15 /PROD=interleukin 15 / DB_XREF=gi:10835152 / UG=Hs_168132 interleukin 15 (IL15), mRNA. / FI=gb:NM_000585.1 gb:U11407.1
203232_s_at	gb:NM_004699.1 /DEF-Homo sapiens DNA segment on chromosome X (unique) 9928 expressed sequence (DXS9928E), mRNA. / FEA=mRNA /GEN=DXS9928E /PROB=XAP-5 protein /DB_XREF=gi:4758219 / UG=Hs_54277 DNA segment on chromosome X (unique) 9928 expressed sequence / FI=gb:BC000028.1 gb:DB81260.1 gb:AD001520.1 gb:NM_004699.1
213337_at	Consensus includes gb:AV10131 /FEA=EST /DB_XREF=gi:101717648 /DB_XREF=est:AV101318 /CLONE=ADAGD10 / UG=Hs_218626 ArcAb1-interacting protein Argbp2
207628_s_at	gb:NM_017528.1 /DEF-Homo sapiens putative methyltransferase (HSN1442), mRNA. /FEA=mRNA /GEN=HSN1442 / PROD=putative methylyltransferase /DB_XREF=gi:8923713 / UG=Hs_15520 putative methylyltransferase / FI=gb:NM_017528.1
201527_at	gb:NM_004231.1 /DEF-Homo sapiens ATPase, vacuolar, 14 kDa (ATP514), mRNA. /FEA=mRNA /GEN=ATP514 /PROD=ATPase, vacuolar, 14 kDa /DB_XREF=gi:1757819 / UG=Hs_78089 AtBase, vacuolar, 14 kDa / FI=gb:D49400.1 gb:NM_004231.1
202282_at	gb:NM_004493.1 /DEF-Homo sapiens hydroxacyl-Coenzyme A dehydrogenase, type II (HADH2), mRNA. /FEA=mRNA /GEN=HADH2 / PROD=hydroxacyl-Coenzyme A dehydrogenase, type II / FI=gb:BC000372.1 gb:NM_004493.1 gb:AE035555.1 gb:NM_004493.1
213735_s_at	Consensus includes gb:AI557312 /FEA=EST /DB_XREF=gi:4489675 /DB_XREF=est:PT2.1_16_E11.r / UG=Hs_1342 cytochrome c oxidase subunit Vb
212472_at	Consensus includes gb:BE965029 /FEA=EST /DB_XREF=est:601658812R1 /CLONE=IMAGE:3886131 /UG=Hs_198793 Homo sapiens cDNA: FI:J22463 , firs, clone HRCJ0126
214805_at	Consensus includes gb:U79273.1 /DEF=Human clone 23933 mRNA sequence. /FEA=mRNA /DB_XREF=gi:1710239 /UG=Hs_239483 Human clone 23933 mRNA sequence
218084_x_at	gb:NM_014164.2 /DEF-Homo sapiens FXID domain-containing ion transport regulator 5 (FXID5), mRNA. /FEA=mRNA /GEN=FXID5 / PROD=related to ion channel /DB_XREF=gi:11612664 / UG=Hs_294135 FXID domain-containing ion transport regulator 5 / FI=gb:NM_014164.2 gb:AF161162.1
218204_s_at	gb:NM_024513.1 /DEF-Homo sapiens FIVe and coiled-coil domain containing 1 (FIVC1), mRNA. /FEA=mRNA /GEN=FIVC1 / PROD=FIVe and coiled-coil domain containing 1 /DB_XREF=gi:1347091 /UG=Hs_257267 FVVE and coiled-coil domain containing 1 / FI=gb:NM_024513.1
200873_x_at	gb:NM_001992.1 /DEF-Homo sapiens ribosomal protein L29 (RPL29), mRNA. /FEA=mRNA /GEN=RPL29 /PROD=ribosomal protein L29 / DB_XREF=gi:1506628 / UG=Hs_183698 ribosomal protein L29 / FI=gb:U49083.1 gb:NM_000982.1 gb:U10248.1
208988_s_at	gb:BC002568.1 /DEF-Homo sapiens, hypothetical protein, clone MGCI2478, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein /DB_XREF=gi:12803484 / UG=Hs_4900 hypothetical protein / FI=gb:AF248964.1 gb:BC002568.1 gb:AF116609.1
208887_at	gb:BC000733.1 /DEF-Homo sapiens, eukaryotic translation initiation factor 3, subunit 4 (Delta, 41kD), clone MGCI2053, mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic translation initiation factor 3, subunit 4 (Delta, 44kD) /DB_XREF=gi:12653882 / UG=Hs_28081 eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD) / FI=gb:AF094850.1 gb:BC000733.1 gb:AF020833.1
214097_at	Consensus includes gb:AW024383 /FEA=EST /DB_XREF=gi:5877913 /DB_XREF=est:wv03e06.x1 /CLONE=IMAGE:2528482 / UG=Hs_1948 ribosomal protein S21

212191_x_at	Consensus includes qb:AW574664 /FEA=EST /DB_XREF=gi:7246203 /DB_XREF=est:UT-HF-BL0-abw-d-10-U-I.s1 /CLONE=IMAGE:3057859 / UG=Is_10842 ribosomal protein L13
217937_at	qb:NM_013242.1 /DEF=Homo sapiens similar to mouse Glt3 or D. melanogaster transcription factor L1B (AF093680), mRNA. /FEA=mRNA /GEN=AF093680 /PROD=similar to mouse Glt3 or D. melanogaster transcription factor L1B /FL=gb:BC0005152.1 qb:NM_013242.1
201658_at	Consensus includes qb:AU151560 /FEA=EST /DB_XREF=gi:11013081 /DB_XREF=est:AU151560 /CLONE=NT2RP2005555 /UG=Hs_242894 ADP-ribosylation factor-like 1 /FL=gb:NM_001177.2 qb:128997.1
218123_at	qb:NM_017835.1 /DEF=Homo sapiens chromosome 21 open reading frame 59 (C21orf59), mRNA. /FEA=mRNA /GEN=C21orf59 /PROD=hypothetical protein FLJ70467 /DB_XREF=gi:18923436 /UG=Hs_5811 chromosome 21 open reading frame 59 /FL=gb:NM_021254.1 qb:BC000709.1 qb:NM_017835.1 qb:AF282851.1
205211_at	qb:NM_005138.1 /DEF=Homo sapiens SCO (cytochrome oxidase deficient, yeast) homolog 2 (SCO2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=SCO2 /PROD=SCO (cytochrome oxidase deficient, yeast) homolog 2 /DB_XREF=gi:1826991 /UG=Hs_278431 SCO (cytochrome oxidase deficient, yeast) homolog 2 /FL=gb:NM_005138.1 qb:NM_0051792.1 /DEF=Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /GEN=MPHOSPH6 /PROD=M-phase phosphoprotein 6 /DB_XREF=gi:5031918 /UG=Hs_152720 M-phase phosphoprotein 6 /FL=gb:BC005242.1 qb:NM_0051792.1
203740_at	qb:NM_031287.1 /DEF=Homo sapiens hypothetical protein MGCI333 (MGCI333), mRNA. /FEA=mRNA /GEN=MGCI333 /PROD=hypothetical protein MGCI333 /DB_XREF=gi:13775199 /FL=gb:NM_031287.1
221263_s_at	qb:NM_0041107.1 /DEF=Homo sapiens FC fragment or IgG, receptor, transporter, alpha (FCERT), mRNA. /FEA=mRNA /GEN=FCERT /PROD=Fc fragment of IgG, receptor, transporter, alpha /FL=gb:NM_004107.1 qb:U12255.1 UG=Hs_111903 FC fragment of IgG, receptor, transporter, alpha /FL=gb:NM_004107.1 qb:U12255.1
201400_at	qb:NM_002795.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, beta type: 3 (PSMB3), mRNA. /FEA=mRNA /GEN=PSMB3 /PROD=proteasome (prosome, macropain) subunit, beta type: 3 /DB_XREF=gi:156196 /UG=Hs_82793 proteasome (prosome, macropain) subunit, beta type: 3 /FL=gb:NM_002795.1 qb:D26598.1
203136_at	qb:NM_006423.1 /DEF=Homo sapiens Rab acceptor 1 (prenylated) (RABAC1), mRNA. /FEA=mRNA /GEN=RABAC1 /PROD=Rab acceptor 1 (prenylated) /DB_XREF=gi:5453939 /UG=Hs_11417 Rab acceptor 1 (prenylated) /FL=gb:NM_006423.1 qb:AF112202.1
205382_s_at	qb:NM_001928.1 /DEF=Homo sapiens D component of complement (adipsin) (DF), mRNA. /FEA=mRNA /GEN=DF /PROD=adipsin/incomplement factor D precursor /DB_XREF=gi:4503308 /UG=Hs_155597 D component of complement (adipsin) /FL=gb:NM_044226.1 qb:NM_001928.1
208714_at	qb:AF021131.1 /DEF=Homo sapiens 51kDa subunit of NADH dehydrogenase mRNA, complete cds. /FEA=mRNA /PROD=51kDa subunit of NADH dehydrogenase /DB_XREF=gi:15136911 /UG=Hs_7744 NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD) /FL=gb:AF021130.1 qb:AF021131.1 qb:NM_007103.1
209224_s_at	qb:BC003674.1 /DEF=Homo sapiens, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8) clone MGC_12315, mRNA, complete cds. /FEA=mRNA /PROD=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8) /FL=gb:BC003674.1 qb:NM_002488.1 qb:AF077029.1
210574_s_at	qb:AF241788.1 /DEF=Homo sapiens NPD011 (NPD011) mRNA, complete cds. /FEA=mRNA /GEN=NPD011 /PROD=NPD011 /DB_XREF=gi:12005192 /UG=Hs_263812 nuclear distribution gene C (A. nidulans) homolog /FL=gb:AF241788.1
214259_s_at	Consensus includes qb:AA14075 /FEA=EST /DB_XREF=gi:3665884 /DB_XREF=est:q163e12.x1 /CLONE=IMAGE:1861198 /UG=Hs_6980 aldo-keto reductase family 7, member A2, leflaxotoxin aldehyde reductase
209234_at	Consensus includes qb:BF939474 /FEA=EST /DB_XREF=gi:12356794 /DB_XREF=est:nac76d12.x1 /CLONE=IMAGE:3440303 /UG=Hs_129808 KIAA0591 protein /FL=gb:BC001415.1
203654_s_at	qb:NM_004645.1 /DEF=Homo sapiens coillin (COIL), mRNA. /FEA=mRNA /GEN=COIL /PROD=coillin / PROD=splicing factor, arginine-serine-rich 7 (35kd) (SFRS7), mRNA. /FEA=mRNA /GEN=SFRS7 / arginine-serine-rich 7 (35kd) /FL=gb:BC000997.2 qb:L22253.1 qb:NM_006276.2
202451_at	qb:BC000365.1 /DEF=Homo sapiens general transcription factor IIH, polypeptide 1 (62kd subunit), clone NGC-8323, mRNA, complete cds. /FEA=mRNA /PROD=general transcription factor IIH, polypeptide 1 (62kd subunit) /DB_XREF=gi:12653194 factor IIH, polypeptide 1 (62kd subunit) /FL=gb:BC000365.1 qb:BC004452.1 qb:NM_0055609.1 qb:NM_005516.1 /UG=Hs_89378 general transcription factor IIH, polypeptide 1 (62kd subunit) /DB_XREF=gi:12653194
218072_at	qb:NM_014186.1 /DEF=Homo sapiens HSPC166 protein (HSPC166), mRNA. /FEA=mRNA /GEN=HSPC166 /PROD=HSPC166 protein /DB_XREF=gi:7661827 /UG=Hs_279836 HSPC166 protein /FL=gb:AL1_36688.1 qb:AF161515.1 qb:NM_014186.1

203063_at	gb:NM_014644.1 / DEF=Homo sapiens KIAA0015 gene product (KIAA0015), mRNA. / FEA=mRNA /GEN=KIAA0015 /PROD=KIAA0015 gene product /DB_XREF=gi:7661861 /UG=Hs.278441 KIAA0015 gene product /FL=gb:D13640.1 gb:NM_014634.1
204037_at	Consensus includes gb:EF055366 / FEA=EST /UG=Hs.75794 endothelial differentiation, Lysophosphatidic acid G-protein-coupled receptor, 2 /FL=gb:U78192.1 gb:NM_001401.1
211298_s_at	gb:NM_024952.1 / DEF=Homo sapiens hypothetical protein FLJ20950 /UG=Hs.1537636 /XREF=gi:11337636 hypothetical protein FLJ20950 /FL=gb:NM_024952.1 /PROD=Hypothetical protein FLJ20950 /DEF=Homo sapiens T-cell, immune regulator 1 ('TCIRG1'), mRNA. / FEA=mRNA /GEN=TCIRG1 /PROD=ATPase, H+ transporting, Na+/K+ /DB_XREF=gi:15174620 /UG=Hs.16465 T-cell, immune regulator 1 /FL=gb:U45285.1 gb:NM_006199.1
203842_s_at	Consensus includes gb:W93187 / FEA=EST /DB_XREF=gi:11429390 /DB_XREF=est:zd06C09.s1 /CLONE=IMAGE:357328 /UG=Hs.6880 DKEFP43D156 protein /FL=gb:BC001408.1
203047_at	gb:NM_005990.1 / DEF=Homo sapiens serine/threonine kinase 10 (STK10), mRNA. / FEA=mRNA /GEN=STK10 /PROD=serine/threonine kinase 10 /DB_XREF=gi:5174700 /UG=Hs.16134 serine/threonine kinase 10 /FL=gb:AB015718.1 gb:NM_005990.1 gb:AEI119894.1
213408_s_at	Consensus includes gb:AK024034.1 / DEF=Homo sapiens CDNA FLJ13972 fis, Clone Y79A0105148, highly similar to PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67). / FEA=mRNA /DB_XREF=gi:10436297 /UG=Hs.171625 phosphatidylinositol 4-kinase, catalytic, alpha polypeptide /PROD=Similar to hypothetical protein FLJ11585, clone MGC:112556, mRNA, complete cds. /FEA=mRNA /PROD=Similar to hypothetical protein FLJ11585 /DB_XREF=gi:112804048 /UG=Hs.315567 Homo sapiens, Similar to hypothetical protein FLJ11585, clone MGC:112558, mRNA, complete cds /FL=gb:BC002877.1
335526_at	Cluster Incl. U3094: Human N-sulphogucosamine sulphohydrolase mRNA, complete cds /cds=[12..1520] /gb=U30894 /gi=1173542 /ug=Hs.31074 /len=1657
203871_s_at	gb:NM_015653.1 / DEF=Homo sapiens ORF (LOC51035), mRNA. / FEA=mRNA /GEN=LOC51035 /PROD=Unknown protein LOC51035 /DB_XREF=gi:7705653 /UG=Hs.77868 ORF /FL=gb:BC000902.1 gb:M68864.1 /gb:NM_015853.1
2121204_at	Consensus includes gb:AI01944.1 / DEF=Homo sapiens mRNA; cDNA DKFZP564G2022 (From clone DKFZP564G2022); partial cds. / FEA=mRNA /GEN=DKEFP564G2022 /PROD=hypothetical protein /DB_XREF=gi:40884189 /UG=Hs.16492 DKEFP564G2022 protein
2171802_s_at	gb:NM_022731.1 / DEF=Homo sapiens similar to rat nuclear ubiquitinous casein kinase 2 (NUCKS), mRNA. / GEN=NUCKS /PROD=similar to rat nuclear ubiquitinous casein kinase 2 /FL=gb:NM_022731.1 gb:BC000805.1
201960_s_at	gb:NM_015057.1 / DEF=Homo sapiens KIAA0916 protein (KIAA0916), mRNA. / FEA=mRNA /GEN=KIAA0916 /PROD=KIAA0916 protein /DB_XREF=gi:7663239 /UG=Hs.15411 KIAA0916 protein /FL=gb:AF05587.1 gb:AF083244.1 gb:NM_015057.1
447608_at	Cluster Incl. AI687401: tq18h09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE:22020217 /clone_end=3 /gb=AI697401 /gi=4985301 /gb:Hs.9741 /len=659
2120250_x_at	gb:AE067854.1 / DEF=Homo sapiens adenylosuccinate lyase (ADSL), mRNA, alternatively spliced, complete cds. / FEA=mRNA /GEN=ADSL /PROD=adenylosuccinate lyase /DB_XREF=gi:13211983 /UG=Hs.75527 adenylosuccinate lyase /FL=gb:AF067854.1
21218495_at	gb:NM_004182.1 / DEF=Homo sapiens ubiquitously-expressed transcript (UTX), mRNA. / FEA=mRNA /GEN=UTX /PROD=ubiquitously-expressed transcript /DB_XREF=gi:4759297 /UG=Hs.117291 ubiquitously-expressed transcript /FL=gb:BC000720.1 gb:AF092737.1 gb:AF04182.1 gb:AF083241.1 gb:AF083242.1
20201106_at	gb:NM_002085.1 / DEF=Homo sapiens glutathione peroxidase 4 (phospholipid hydroperoxidase) (GPX4), mRNA. / FEA=mRNA /GEN=GPX4 /PROD=glutathione peroxidase 4 /DB_XREF=gi:4504106 /UG=Hs.2706 glutathione peroxidase 4 (phospholipid hydroperoxidase) /FL=gb:NM_002085.1
20203569_s_at	gb:NM_003611.1 / DEF=Homo sapiens chromosome X open reading frame 5 /DB_XREF=gi:4503178 /UG=Hs.6483 oral-facial-digital syndrome 1 gene /FL=gb:NM_003611.1
20201316_at	Consensus includes gb:AL523904 / FEA=EST /DB_XREF=gi:12787397 /DB_XREF=est:AL523904 /CLONE=CSDC033YB07 (3 prime) /PROD=chromosome X open reading frame 5 /GEN=ADSR /PROD=adenylosuccinate lyase /alpha type, 2 /FL=gb:NM_002787.1
21218336_at	gb:NM_012394.2 / DEF=Homo sapiens prefoldin 2 (PFDN2), mRNA. / FEA=mRNA /GEN=PFDN2 /PROD=prefoldin 2 /DB_XREF=gi:12408674 /UG=Hs.295229 Prefoldin 2 /FL=gb:NM_012394.2 gb:AF165883.1 gb:AF17237.1 gb:AF151065.1
209370_s_at	Consensus includes gb:BP502377 / FEA=EST /DB_XREF=gi:9704785 /DB_XREF=est:hy22903.x1 /CLONE=IMAGE:3198100 /UG=Hs.167679 SH3-domain binding protein 2 /FL=gb:AB00462.1 gb:AF00936.1
201036_s_at	gb:NM_005327.1 / DEF=Homo sapiens L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (HADHSC), mRNA. / FEA=mRNA /PROD=L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /DB_XREF=gi:4885386 /UG=Hs.8110 L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /FL=gb:BC000306.1 gb:NM_005327.1
087716_at	Consensus includes gb:BF132873 / FEA=EST /DB_XREF=est:7n28a02.x1 /CLONE=IMAGE:3565730 /UG=Hs.90744 proteosome

21475_s_at	(prosome, macropain) 26S subunit, non-ATPase, 11 / <i>El</i> =gb:BC000437.1 qb:AB003102.1 qb:AF01212.1 qb:NM_002815.1
Consensus includes qb:AK024671.1 /DEF=Homo sapiens cDNA: FLJ21024 <i>fis</i> , clone CAG06651, highly similar to HMP1T Human LTR mRNA. /FEA=mRNA /DB_XREF=gi:1043016 /UG-Hs_264330 N-acylsphingosine amidohydrolase (acid ceramidase)-like protein / <i>El</i> =gb:NM_006037.2 / <i>El</i> =gb:Hs_9100 histone deacetylase 4 / <i>El</i> =gb:NM_006037.2 qb:AF0132607.1	
204225_at	Consensus includes qb:AA669797 /FBA=EST /DB_XREF=gi:12631296 /DB_XREF=est:ag3tc01.s1 /CLONE=IMAGE:1118880 /UG=Hs_75633 fumurate hydratase
218652_s_at	gb:NM_024619.1 /DEF=Homo sapiens hypothetical protein FLJ12171, mRNA, /FEA=mRNA /GEN=FLJ12171 /PROD=hypothetical protein FLJ12171 /DB_XREF=gi:13375839 /UG-Hs_31431 hypothetical protein FLJ12171 / <i>El</i> =gb:NM_024619.1
212700_x_at	gb:NM_017733.1 /DEF=Homo sapiens hypothetical protein FLJ20265 (FLJ20265), mRNA, /FEA=mRNA /GEN=FLJ20265 /PROD=hypothetical protein FLJ20265 / <i>El</i> =gb:BC001249.1 qb:BC000937.2 qb:NM_017733.1
203906_at	gb:NM_015332.1 /DEF=Homo sapiens protein KIAA0168, mRNA, /FEA=mRNA /GEN=KIAA0168 /PROD=KIAA0168 protein /DB_XREF=gi:13357209 /UG=Hs_4770 KIAA0168 protein / <i>El</i> =gb:BC003691.1 qb:NM_015332.1
221516_s_at	Consensus includes qb:AI652645 /FBA=EST /DB_XREF=gi:1736624 /DB_XREF=est:wb30b07.x1 /CLONE=IMAGE:2307157 /UG=Hs_4764 KIAA0763 gene product / <i>El</i> =gb:AB018306.1 qb:NM_014863.1
203492_x_at	gb:BC002581.1 /DEF=Homo sapiens hypothetical protein / <i>El</i> =gb:BC002581.1
212048_s_at	gb:NM_013679.1 /DEF=Homo sapiens ATP synthase, H ₊ transporting, mitochondrial F0 complex, subunit e, clone MGC:12532, mRNA, complete cds. /FEA=mRNA /PROD=ATP synthase, H ₊ transporting, mitochondrial F0 complex, subunit e / <i>El</i> =gb:BC003679.1.
204214_s_at	Consensus includes gb:AW245400 /FBA=EST /DB_XREF=gi:6588393 /DB_XREF=est:2B22751.3prime /CLONE=IMAGE:2822751 /UG=Hs_239307 tetroxyl-tRNA synthetase
217796_s_at	gb:NM_017731.1 /DEF=Homo sapiens oncogene family (RAB32), member RAS oncogene family / <i>El</i> =gb:U1127.1 qb:NM_006834.1
203327_at	Consensus includes gb:N22903 /FBA=EST /DB_XREF=est:yx6604..81 /CLONE=IMAGE:266718 /UG=Hs_1508 insulin-degrading enzyme / <i>El</i> =gb:M21188.1 qb:NM_004969.1
208659_at	qb:AF034607.1 /DEF=Homo sapiens chloride channel ABP mRNA, complete cds. /FEA=mRNA /PROD=chloride channel ABP /DB_XREF=gi:4426566 / <i>El</i> =gb:NM_74216 chloride intracellular channel 1 / <i>El</i> =gb:U93205.1 qb:AF034607.1 qb:AF109197.1 qb:NM_001288.2
222218_s_at	Consensus includes qb:AJ100813.1 /DEF=Homo sapiens partial mRNA for immunoglobulin-like cell surface receptor FDF03-M14, soluble immunoglobulin-like receptor alpha
211862_x_at	qb:AF015451.1 /DEF=Homo sapiens Urspin-beta mRNA, complete cds. /FEA=CDS /PROD=Uspurpin-beta /DB_XREF=gi:3133282 /UG=Hs_195175 CASP8 and FADD-like apoptosis regulator / <i>El</i> =gb:AF015451.1
209080_x_at	qb:AF118552.1 /DEF=Homo sapiens PKC ζ -interacting protein PICOT (PICOT) mRNA, complete cds. /FEA=mRNA /GEN=PILOT /PROD=PKC ζ -interacting protein PICOT / <i>El</i> =gb:BC05280.1 qb:AF118549.1 qb:AF118632.1
200789_at	gb:NM_001398.1 /DEF=Homo sapiens enoyl Coenzyme A hydrolase 1, Peroxisomal (ECH1), mRNA, /FEA=mRNA /GEN=ECH1 /PROD=peroxisomal enoyl-CoA-hydrolase-like protein / <i>El</i> =gb:NM_196176 enoyl Coenzyme A hydratase 1, peroxisomal / <i>El</i> =gb:NM_001398.1 qb:U16660.1
90610_at	Cluster incl. AF054877:wb65b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2310523 /clone_end=3 /qb=AF1654857 /gi=4738836 /ug=Hs_160115 /len=621
201704_at	gb:NM_001247.1 /DEF=Homo sapiens ectonucleoside triphosphate diphosphohydrolase 6 (putative function) (ENTPD6), mRNA, /FEA=mRNA /GEN=ENTPD6 /PROD=ENTPD6 / <i>El</i> =gb:NM_12330 ectonucleoside triphosphate diphosphohydrolase 6 (putative function) /DB_XREF=gi:4557422 / <i>El</i> =gb:Hs_12330
218026_at	gb:NM_014019.1 /DEF=Homo sapiens HSPC009 protein (HSPC009), mRNA, /FEA=mRNA /GEN=HSPC009 /PROD=HSPC009 protein /DB_XREF=gi:7661731 /UG=Hs_16059 HSPC009 protein / <i>El</i> =gb:BC002698.1 qb:AF070655.1 qb:NM_014019.1
214771_x_at	Consensus includes qb:AK025604.1 /DEF=Homo sapiens cDNA: FLJ21951 <i>fis</i> , clone HSP04968. /FEA=mRNA /DB_XREF=gi:10438172 / <i>El</i> =gb:Hs_84883 KIAA0864 protein
208760_at	Consensus includes qb:AD03114 /DEF=Human DNA sequence from clone IAI6-35887 on chromosome 16 Contains the UBB21 gene for ubiquitin-conjugating enzyme E21 (homologous to yeast OBC9), and an RBS20 (40S Ribosomal protein S20) pseudogene. Contains ESTs, STSs, GSSs and a putative CpG is... /FEA=mRNA /DB_XREF=gi:475508 /UG=Hs_84285 ubiquitin-conjugating enzyme E21 (homologous to

yeast UBC9) /FI=gb:U45328.1 gb:U31933.1 gb:BC000427.1 gb:U66818.1 gb:U66867.1 gb:U38785.1 gb:NM_003345.1 gb:U20992.1
Consensus includes gb:IN3526 /FEA=EST /DB_XREF=gi:1152925 /DB_XREF=est:yy11f04 .S1 /CLONE=IMAGE:Z10943 /UG=Hs_30642 serologically defined colon cancer antigen 8
Cluster Incl. A142320:tJ8t02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE:2148482 /clone_end=3 /gb=AI472320 /gi=4334410 / ug=Hs_48504 /len=548
205819_at gb:NM_00670.1 /DEF=Homo sapiens macrophage receptor with collagenous structure /DB_XREF=gi:5803079 /UG=Hs_67726 macrophage receptor with collagenous structure /FI=gb:AF035819.1 qb:NM_00670.1
218019_s_at gb:NM_02941.1 /DEF=Homo sapiens hypothetical protein FLJ21324 /mRNA, /FEA=mRNA /GEN=FLJ21324 /PROD=hypothetical protein FLJ21324 /FI=gb:NM_021941.1 qb:NM_021941.1
219220_x_at gb:NM_020191.1 /DEF=Homo sapiens protein (GK002) /mRNA, /FEA=mRNA /GEN=GK002 /PROD=GK002 protein /DB_XREF=gi:9910243 / ug=Hs_101027 GK002 protein; qibt protein; chromosome 3 open reading frame 5 /FI=gb:AF321613.1 qb:NM_020191.1
212355_at Consensus includes gb:AI075450 /FEA=EST /DB_XREF=gi:13399805 /DB_XREF=est:o282g10.x1 /CLONE=IMAGE:1681890 / ug=Hs_7911 KIAA0232 protein
214735_at Consensus includes gb:AW166711 /FEA=EST /DB_XREF=gi:6398236 /DB_XREF=est:xg27h02.x1 /CLONE=IMAGE:2628819 / ug=Hs_181440 KIAA0403 protein
219041_s_at gb:NM_01374.1 /DEF=Homo sapiens zinc finger protein (AP4), mRNA, /FEA=mRNA /GEN=AP4 /PROD=zinc finger protein / DB_XREF=gi:7656889 /UG=Hs_90593 zinc finger protein /FI=gb:EC000363.1 qb:NM_014374.1
209110_s_at gb:AL050559.1 /DEF=Homo sapiens mRNA; cDNA DKF2p564D0782 (from clone DKF2p564D0782); complete cds. /FEA=mRNA /GEN=DKF2p564D0782 / PROD=hypothetical protein /DB_XREF=gi:4886416 /UG=Hs_170160 RAB2, member RAS oncogene family-like /FI=gb:DB5757.1 qb:NM_004761.1 gb:AL050559.1
215691_x_at Consensus includes gb:AV702984 /FEA=EST /DB_XREF=est:AV702994 /CLONE=ADABSB06 /UG=Hs_46967 HSPC034 protein
207614_s_at gb:NM_005692.1 /DEF=Homo sapiens cullin 1 (CUL1), mRNA, /FEA=mRNA /GEN=CUL1 /PROD=cullin 1 /DB_XREF=gi:4503160 / ug=Hs_14341 cullin 1 /FI=gb:U58087.1 qb:NM_00352.1
213405_at Consensus includes gb:IN95443 /FEA=EST /DB_XREF=gi:1267753 /DB_XREF=est:zb8ic12.s1 /CLONE=IMAGE:310006 /UG=Hs_19180 Homo sapiens mRNA; cDNA DKF2p564E122 (from clone DKF2p564E122)
208835_s_at Consensus includes gb:AV089673 /FEA=EST /DB_XREF=gi:6047017 /DB_XREF=est:xk21h11.x1 /CLONE=IMAGE:2594169 /UG=Hs_3688 cisplatin resistance-associated overexpressed protein /FI=gb:AB034205.1
202225_at Consensus includes gb:AV61231 /FEA=EST /DB_XREF=gi:7317497 /DB_XREF=est:ng95e07.x1 /CLONE=IMAGE:2953380 /UG=Hs_306088 v-crk avian sarcoma virus CT10 oncogene homolog /FI=gb:D10656.1 qb:NM_016823.1
218338_at gb:NM_02324.1 /DEF=Homo sapiens hypothetical protein MGC11256 (MGC11256) , mRNA, /FEA=mRNA /GEN=MGC11256 /PROD=hypothetical protein MGC11256 /DB_XREF=gi:13236568 /UG=Hs_28029 hypothetical protein MGC11256 /FI=gb:BCU02894.1 qb:NM_024324.1
213551_s_at Consensus includes gb:AI167164 /FEA=EST /DB_XREF=est:sg08c10.x1 /CLONE=IMAGE:1565386 /UG=Hs_23200 myotubularin related protein 1
218133_s_at gb:NM_021824.1 /DEF=Homo sapiens NIF3 (Nifg1 interacting factor 3, S.pombe homolog)-like 1 /DB_XREF=gi:1141898 /UG=Hs_21943 NIF3 (Nifg1 interacting factor 3, S.pombe homolog)-like 1 /FI=gb:AF182416.1 qb:NM_021824.1 qb:AF60513.1 qb:AB038949.1
212007_at Consensus includes gb:AI927512 /FEA=EST /DB_XREF=gi:15633476 /DB_XREF=est:ng90c11.x1 /CLONE=IMAGE:2462660 /UG=Hs_77495 UBX domain-containing 1
204650_at gb:NM_004853.1 /DEF=Homo sapiens syntaxin 8 (STX8) , mRNA, /FEA=mRNA /GEN=STX8 /PROD=syntaxin 8 /DB_XREF=gi:4759187 /UG=Hs_119525 syntaxin 8 /FI=gb:AF036715.1 qb:NM_004853.1
210042_s_at gb:AF073890.1 /DEF=Homo sapiens cathepsin X precursor, mRNA, complete cds. /FEA=mRNA /PROD=cathepsin X precursor / DB_XREF=gi:3650497 /UG=Hs_252549 cathepsin Z /FI=gb:AF032906.1 qb:AF03890.1 qb:NM_001336.1 qb:AF136273.1
32091_at Cluster Incl. AB007915:Homo sapiens mRNA for KIAA046 protein, complete cds /cds=(3531,4286) /gb=AB007915 /gi=3413853 / ug=Hs_158286 /len=644
201135_at gb:NM_004092.2 /DEF=Homo sapiens enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (ECHS1) , nuclear gene encoding mitochondrial protein, mRNA, /FEA=mRNA /GEN=ECHS1 /PROD=mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor / DB_XREF=gi:12707569 /UG=Hs_76394 enoyl Coenzyme A hydratase, short chain, 1, mitochondrial /FI=gb:NM_004092.2 qb:DL3300.1
220556_s_at gb:NM_017971.1 /DEF=Homo sapiens hypothetical protein FLJ10024 (FLJ10024) , mRNA, /FEA=mRNA /GEN=FLJ10024 /PROD=hypothetical protein FLJ10024 /DB_XREF=gi:8322189 /UG=Hs_182698 hypothetical protein FLJ10024 /FI=gb:NM_017971.1

208308_s_at	gb:NM_000175.1 /DEF=Homo sapiens glucose phosphate isomerase (GPI), mRNA. /FEA=mRNA /GEN=GPI /PROD=glucose phosphate isomerase /
208429_x_at	gb:AF112207.1 /DEF=Homo sapiens translation initiation factor eIF-2b delta subunit /DB_XREF=gi:6563201 /UG=Hs_169474 DKTP586J0119 protein /
221501_x_at	gb:AF229059.1 /DEF=Homo sapiens KIAA0220-like protein mRNA, complete cds. /FEA=mRNA /PROD=KIAA0220-like protein /
209161_at	DB_XREF=gi:8980670 /UG=Hs_251928 nuclear pore complex interacting protein /FL=gb:AF229059.1 /CLONE=IMAGE:1724694 /UG=Hs_8551 PRP4STIKWD
209161_s_at	Consensus includes gb:AF112207.1 /DEF=Homo sapiens translation initiation factor eIF-2b delta subunit /DB_XREF=est:qd24904.x1 /CLONE=IMAGE:1724694 /UG=Hs_8551 PRP4STIKWD
201414_s_at	gb:NM_005369.1 /DEF=Homo sapiens nucleosome assembly protein 1-like 4 (NP114), mRNA. /FEA=mRNA /GEN=NAP1L4 /
212361_s_at	PRODenucleosome assembly protein 1-like 4 /DB_XREF=gi:5174612 /UG=Hs_78103 nucleosome assembly protein 1-like 4 /
212361_s_at	FL=gb:U77456.1 /gb:NM_005369.1
204084_s_at	Consensus includes gb:AF1190070 /FEA=EST /DB_XREF=gi:6464550 /DB_XREF=est:xx11f11.x1 /CLONE=IMAGE:2675949 /UG=Hs_15226 AtBase, Cat+, transporting, cardiac muscle, slow twitch 2
203200_s_at	Consensus includes gb:AF11911687 /FEA=EST /DB_XREF=est:wc7q01.x1 /CLONE=IMAGE:2324112 /UG=Hs_30213
201405_s_at	gb:NM_006633.1 /DEF=Homo sapiens COP9 subunit 6 (MOV34 homolog, 34 kD) (MOV34 /34KD), mRNA. /FEA=mRNA /GEN=Mov34-34KD /
218556_at	PROD=COP9 subunit 6 (MOV34 homolog, 34 kD) /DB_XREF=gi:5803095 /UG=Hs_15591 COP9 subunit 6 (MOV34 homolog, 34 kD) /
217756_x_at	gb:NM_014182.1 /DEF=Homo sapiens HSPC160 protein (HSPC160), mRNA. /FEA=mRNA /PROD=HSPC160 protein /
208983_s_at	DB_XREF=gi:18661819 /UG=Hs_13144 HSPC160 protein /FL=gb:AF1161509.1 /gb:NM_014182.1
202026_at	gb:NM_005770.1 /DEF=Homo sapiens small EDRK-rich factor 2 (SERF2), mRNA. /FEA=mRNA /GEN=SERF2 /PROD=small EDRK-rich factor 2 /
212165_at	Consensus includes gb:AV701283 /FEA=EST /DB_XREF=gi:10717613 /DB_XREF=est:AV701283 /CLONE=ADACR06 /UG=Hs_50785 SEC22, vesicle trafficking protein (S. cerevisiae)-like 1 /FL=gb:BC001364.1 /gb:NM_00492.1
202042_at	gb:NM_002109.2 /DEF=Homo sapiens histidyl-tRNA synthetase (HARS), mRNA. /FEA=mRNA /GEN=HARS /PROD=histidyl tRNA synthetase /
202433_at	DB_XREF=gi:6996013 /UG=Hs_77798 histidyl-tRNA synthetase /FL=gb:NM_002109.2
201145_at	gb:NM_005827.1 /DEF=Homo sapiens UDP-galactose transporter related (UGTRELL1), mRNA. /FEA=mRNA /GEN=UGTRELL1 /
C11975_at	gb:NM_005827.1 /DEF=UDP-galactose transporter related /DB_XREF=gi:5803222 /UG=Hs_154073 UDP-galactose transporter related /FL=gb:D87989.1
200918_s_at	gb:NM_006118.2 /DEF=Homo sapiens HSI binding protein (HAX1), mRNA. /FEA=mRNA /GEN=HAX1 /PROD=HS1 binding protein /
203497_at	DB_XREF=gi:13435355 /UG=Hs_15318 HSI binding protein /FL=gb:NM_006118.2 /gb:BC005240.1 /gb:U88566.1
209153_s_at	Consensus includes gb:BE299671 /FEA=EST /DB_XREF=gi:9183419 /DB_XREF=est:6009443421 /CLONE=IMAGE:2960218 /
220956_x_at	gb:NM_256310 Protein kinase C and casein kinase substrate in neurons 3
	gb:NM_005139.1 /DEF=Homo sapiens signal recognition particle receptor (docking protein) (SRPR), mRNA. /FEA=mRNA /GEN=SRPR /
	PROD=signal recognition particle receptor (docking protein) /DB_XREF=gi:4507222 /UG=Hs_75730 signal recognition particle receptor (docking protein) /FL=gb:BC001162.1 /gb:NM_005139.1
	gb:NM_004774.1 /DEF=Homo sapiens PPAR binding protein (PPARBP), mRNA. /FEA=mRNA /GEN=PPARBP /PROD=thyroid hormone receptor interactor 2 /DB_XREF=gi:4759265 /UG=Hs_15389 PPAR binding protein /FL=gb:FE055994.1 /gb:NM_004774.1 /gb:AF283812.1
	gb:NM_01523.1 /DEF=Human transcription factor (E2A) mRNA, complete cds. /FEA=mRNA /GEN=TCF3 /DB_XREF=gi:3339477 /UG=Hs_101047
	transcription factor 3 (E2A) immunoglobulin enhancer binding factors E12E47, /FL=gb:M31523.1
	gb:NM_030978.1 /DEF=Homo sapiens hypothetical protein similar to actin related protein 23 complex subunit 5 (MGC30381), mRNA. /FEA=mRNA /GEN=MGC30381 /
	FL=gb:NM_030978.1

212705_s_at	Consensus includes gb:AA160181 / FEA=EST / DB_XREF=gi:11734757 / DB_XREF=est:z081d09.s1 / CLONE=IMAGE:593297 / UG=Hs.2'8635 HDMW1BP protein.
219176_at	gb:NM_024520.1 / DEF=Homo sapiens hypothetical protein FLJ22555 (FLJ22555), mRNA. /FEA=mRNA /GEN=FLJ22555 / PROD=hypothetical protein FLJ22555 /DB_XREF=gi:13375659 /UG=Hs.3592 hypothetical protein LOC51160 /mRNA. /GEN=LOC51160 /PROD=vPS28 protein /DB_XREF=gi:116208.1 /DEF=Homo sapiens VPS28 protein (LOC51160), mRNA. /FEA=mRNA /GEN=FLJ22555 / PROD=vPS28 protein /DB_XREF=gi:116208.1
218679_s_at	gb:NM_016208.1 / DEF=Homo sapiens VPS28 protein (LOC51160), mRNA. /FEA=mRNA /GEN=FLJ22555 / PROD=vPS28 protein /DB_XREF=gi:1705884 /UG=Hs.283441. VPS28 protein /FL=gb:AF316887.1 qb:NM_016208.1
206931_s_at	gb:NM_000579.1 / DEF=Homo sapiens chemokine (C-C motif) receptor 5 (CCR5), mRNA. /FEA=mRNA /GEN=CCRS / PROD=chemokine (C-C motif) receptor 5 (CCR5), mRNA. /FEA=mRNA /GEN=CCRS / PROD=chemokine (C-C motif) receptor 5 (CCR5), mRNA. /FEA=mRNA /GEN=FLJ22555 / PROD=putryophilin /DB_XREF=gi:100579.1
209770_at	gb:NM_009555.1 / DEF=Human butyrophilin (BTP5) mRNA, complete cds. /FEA=mRNA /GEN=BTP5 / PROD=butyrophilin /DB_XREF=gi:100555.1 /UG=Hs.284283 butyrophilin, subfamily 3, member A1 /FL=gb:U05552.1
214228_s_at	Consensus includes gb:AL042220 / FEA=EST / DB_XREF=gi:5421564 /DB_XREF=est:DKFZp434H1920_s1 / CLONE=DKFZp434H1920_s1 /CLONE=IMAGE:593297 / PROD=calmodulin related protein 4 myotubularin related protein 4
201885_s_at	gb:NM_000398.3 / DEF=Homo sapiens diaphorase (NADH) (cytochrome b-5 reductase) (DIAL), nuclear gene encoding mitochondrial protein, transcript variant M, mRNA. /FEA=mRNA /GEN=DIAL / PROD=cytochrome b5 reductase, membrane-bound isoform /DB_XREF=gi:6552326 /UG=Hs.274464 diaphorase (NADH) (cytochrome b-5 reductase) /EL=gb:BG004821.1 qb:NM_000398.3
209688_s_at	gb:BC005078.1 / DEF=Homo sapiens, clone MGCA13033, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGCA13033) / DB_XREF=gi:13477224 /UG=Hs.26118 Homo sapiens clone 24166 mRNA sequence /TLI=gb:BC005078.1
203487_s_at	gb:NM_015396.1 / DEF=Homo sapiens DKFZp434A043 protein (DKFZp434A043), mRNA. /FEA=mRNA /GEN=DKFZp434A043 / PROD=DKFZp434A043 protein /DB_XREF=gi:1661561 /UG=Hs.102108 DKFZp434A043 protein /FL=gb:NM_015396.1
202155_s_at	gb:NM_005085.1 / DEF=Homo sapiens nucleoporin 214kd (CAIN) (NUF214), mRNA. /FEA=mRNA /GEN=NUP214 / PROD=nucleoporin 214kd (CAIN) /DB_XREF=gi:8826873 /FL=gb:NM_005085.1
221786_at	Consensus includes gb:BE197222 / FEA=EST / DB_XREF=gi:11085906 /DB_XREF=est:7m88bb07.x1 / CLONE=IMAGE:3561949 /UG=Hs.12312 Homo sapiens Clone 24538 mRNA sequence
212846_at	Consensus includes gb:AA811192 / FEA=EST / DB_XREF=gi:2880803 /DB_XREF=est:zb72808.s1 / CLONE=IMAGE:1336887 /UG=Hs.152629 KIAA0179 protein
209444_at	gb:BC001851.1 / DEF=Homo sapiens, similar to RAP1, GTP-GDP dissociation stimulator 1, clone MGCA14525, mRNA, complete cds. / FEA=mRNA /PROD=Similar to RAP1, GTP-GDP dissociation stimulator 1 /FL=gb:NM_021159.1 qb:BC001851.1 qb:BC001816.1 qb:AE215923.1 qb:AF237413.1
211937_at	Consensus includes gb:NM_001417.1 / DEF=Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA. /FEA=cds / GEN=EIF4B / PROD=eukaryotic translation initiation factor 4B (EIF4B), mRNA. /PROD=polypeptide I (7.6kd), clone MGCA14494, mRNA, complete cds. / FEI=cds / PROD=polypeptide I (7.6kd), clone MGCA14494, mRNA, complete cds. / PROD=deoxyribonuclease
201800_s_at	gb:AF185996.1 / DEF=Homo sapiens oxysterol-binding protein 1 (OBSP21) mRNA, complete cds. /FEA=mRNA /GEN=OBSP21 / PROD=oxysterol-binding protein 1 /DB_XREF=gi:10441379 /UG=Hs.24734 oxysterol binding protein /FL=gb:AF185996.1 qb:M86917.1 qb:NM_002556.1
211730_s_at	gb:BC005903.1 / DEF=Homo sapiens, polymerase (RNA) II (DNA directed) polypeptide I (7.6kd), clone MGCA14494, mRNA, complete cds. / FEA=mRNA /PROD=polymerase (RNA) II (DNA directed) polypeptide I (7.6kd), clone MGCA14494, mRNA, complete cds. / PROD=deoxyribonuclease
65635_at	Cluster Incl. Al044097:DKFZp434M1928_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434M1928 /clone_end=3 /gb:Al044097 /gi=5432324 / ug:Hs.29288 /len=605
207438_s_at	gb:NM_005701.1 / DEF=Homo sapiens RNA, U transporter 1 (RNT1), mRNA. /FEA=mRNA /GEN=RNT1 / PROD=RNA, U transporter 1 / DB_XREF=gi:15039832 /UG=Hs.21577 RNA, U transporter 1 /FL=gb:AF030929.1 qb:NM_005701.1
221819_at	Consensus includes gb:BF791960 / FEA=EST /DB_XREF=gi:12097014 /DB_XREF=est:602252342FL / CLONE=IMAGE:4344539 /UG=Hs.94308 Homo sapiens cDNA FLJ10447 firs, clone NT2RP100851
203912_s_at	gb:NM_006730.1 / DEF=Homo sapiens deoxyribonuclease I-like 1 (DNASE1LL1), mRNA. /FEA=mRNA /GEN=DNASE1LL1 / PROD=deoxyribonuclease I-like 1. Homo sapiens cDNA FLJ11495 firs, clone HEMBA1001950, highly similar to Homo sapiens mRNA for KIAA0971 protein. /FEA=mRNA /DB_XREF=gi:10432760 /UG=Hs.84149 KIAA0971 protein
216996_s_at	gb:NM_006503.2 / DEF=Homo sapiens JTV1 gene (JTV1), mRNA. /FEA=mRNA /GEN=JTV1 / PROD=JTV1 /DB_XREF=gi:111125769 /UG=Hs.301613 JTV1 gene /FL=gb:NM_006503.2 qb:U21169.1 qb:BC02553.1
202138_x_at	gb:NM_024647.1 / DEF=Homo sapiens hypothetical protein FLJ13287 (FLJ13287), mRNA. /FEA=mRNA /GEN=FLJ13287 / PROD=hypothetical protein FLJ13287 /DB_XREF=gi:13375688 /UG=Hs.53263 hypothetical protein FLJ13287 / PROD=hypothetical protein FLJ13287 /DB_XREF=gi:10053263
2119007_at	gb:NM_018398.1 / DEF=Homo sapiens calcium channel alpha2-delta3 subunit (HSA272268), mRNA. /FEA=mRNA /GEN=HSA272268 / PROD=calcium channel alpha2-delta3 subunit /DB_XREF=gi:8923764 /UG=Hs.22958 calcium channel, voltage-dependent, alpha 2delta 3
219714_s_at	gb:NM_018398.1 / DEF=Homo sapiens calcium channel alpha2-delta3 subunit /DB_XREF=gi:8923764 /UG=Hs.22958 calcium channel, voltage-dependent, alpha 2delta 3

		subunit / <i>FI=gb:NM_018398.1</i>
201263_at	gb:NM_003191.1 /DEF=Homo sapiens threonyl-tRNA synthetase (TARS) mRNA. /FEA=mRNA /GEN=TARS /PROD=threonyl-tRNA synthetase /DB_XREF=gi:4507366 /UG-Hs.84131 threonyl-tRNA synthetase /FI=gb:BC000517.1 gb:NM_003191.1	
201157_s_at	Consensus includes <i>gb:AF020500.1</i> /DEF=Homo sapiens myristoyl CoA:protein N-myristoyltransferase mRNA, complete cds. /FEA=CDS /PROD=myristoyl CoA:protein N-myristoyltransferase /DB_XREF=gi:2760893 /UG-Hs.111039 N-myristoyltransferase 1 / <i>FI=gb:NM_021079.1</i> /DEF=Homo sapiens similar to ribosomal protein L31, clone MGC:1641, mRNA, complete cds. /FEA=mRNA /PROD=Similar to ribosomal protein L31 /DB_XREF=gi:12804504 /UG-Hs.164170 vascular Rab-GAPtBc-containing /FI=gb:BC001663.1	
221593_s_at	Consensus includes <i>gb:NM_003664.1</i> /DEF=Homo sapiens adaptor-related protein complex 3, beta 1 subunit /FI=gb:U91504.1 gb:NM_003664.1 /GEN=AP2B1 /PROD=adaptor-related protein complex 3, beta 1 subunit /FI=gb:U91504.1 gb:NM_003664.1	
214202_at	mRNA from chromosome 5q21-22, clone:357Ex /UG-Hs.155372 adaptor-related protein complex 3, beta 1 subunit /FI=gb:NM_003664.1 /DB_XREF=est:yx50h10.x1 /CLONE=IMAGE:265219 /UG-Hs.26968 Homo sapiens	
203142_s_at	Consensus includes <i>gb:NM_00160126</i> /DEF=EST /DB_XREF=gi:3693506 /DB_XREF=est:ab51n08.x1 /CLONE=IMAGE:1703679 /UG-Hs.295901	
222001_x_at	KIAA0493 protein	
213374_x_at	Consensus includes <i>gb:NM_000964</i> /DEF=EST /DB_XREF=gi:5847880 /DB_XREF=est:wr90h10.x1 /CLONE=IMAGE:2495011 /UG-Hs.236642	
201018_at	Consensus includes <i>gb:AL079283.1</i> /DEF=Homo sapiens mRNA full length insert cDNA clone EUROMAGE:39515. /FEA=mRNA /DB_XREF=gi:5102744 /UG-Hs.4310 eukaryotic translation initiation factor 1A /FI=gb:BC000793.1 gb:NM_001412.1	
206206_at	gb:NM_005582.1 /DEF=Homo sapiens lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kD (LY64), mRNA. /FEA=mRNA /GEN=Ly64 /PROD=lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kD /DB_XREF=gi:503189 /UG-Hs.87205 lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kD /FI=gb:D83597.1 gb:NM_005582.1	
209566_at	Consensus includes <i>gb:AL080184.1</i> /DEF=Homo sapiens mRNA; cDNA DKFZp4340071 (from clone DKFZp4340071). /FEA=mRNA /DB_XREF=gi:5262661 /UG-Hs.1089 insulin induced protein 2 /FI=gb:AEI25392.1	
212194_s_at	Consensus includes <i>gb:AI418892</i> /DEF=EST /DB_XREF=gi:4264823 /DB_XREF=est:tf43c01.x1 /CLONE=IMAGE:2098944 /UG-Hs.79305 KIAA0255 gene product	
204526_s_at	gb:NM_007063.1 /DEF=Homo sapiens vascular Rab-GAPtBc-containing (VRP) mRNA. /FEA=mRNA /GEN=VRP /PROD=vascular Rab-GAPtBc-containing /DB_XREF=gi:5902153 /UG-Hs.164170 vascular Rab-GAPtBc-containing /FI=gb:AB24057.1 gb:NM_007063.1	
201558_at	gb:NM_014402.1 /DEF=Homo sapiens low molecular mass ubiquinone-binding protein (9.5kD) (QF-C), mRNA. /FEA=mRNA /GEN=QF-C /PROD=low molecular mass ubiquinone-binding protein /DB_XREF=gi:7657485 /UG-Hs.3709 low molecular mass ubiquinone-binding protein (9.5kD) /FI=gb:BC001390.1 gb:NM_014402.1	
221829_s_at	Consensus includes <i>gb:AI307759</i> /DEF=EST /DB_XREF=gi:4002363 /DB_XREF=est:tb24g08.x1 /CLONE=IMAGE:2055326 /UG-Hs.168075 karyopherin (importin) beta 2	
200653_at	gb:NM_004068.1 /DEF=Homo sapiens adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA. /FEA=mRNA /GEN=AP2M1 /PROD=adaptor-related protein complex 2, mu 1 subunit /DB_XREF=gi:4157993 /UG-Hs.152936 adaptor-related protein complex 2, mu 1 subunit /FI=gb:U36188.1 gb:BC004986.1 gb:D63475.1 gb:NM_004068.1	
213160_at	Consensus includes <i>gb:DE6964.1</i> /DEF=Human mRNA for KIAA0209 gene, partial cds. /FEA=mRNA /GEN=KIAA0209 /DB_XREF=gi:1504001 /UG-Hs.17211 dedicator of cyto-kinesis 2	
211375_s_at	gb:AF111870.1 /DEF=Homo sapiens translational control protein 80 mRNA, complete cds. /FEA=mRNA /PROD=translational control protein 80 /DB_XREF=gi:5006601 /UG-Hs.256583 interleukin enhancer binding factor 3, 90kD /FI=gb:AF141870.1	
202276_at	gb:NM_006304.1 /DEF=Homo sapiens deleted in split-hand-split-foot 1 region (DSS1), mRNA. /FEA=mRNA /GEN=DSS1 /PROD=deleted in split-hand-split-foot 1 region /DB_XREF=gi:5453639 /UG-Hs.85215 Deleted in split-hand-split-foot 1 region /FI=gb:U41515.1	
201892_s_at	gb:NM_000804.1 /DEF=Homo sapiens IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2), mRNA. /FEA=mRNA /GEN=IMPDH2 /PROD=IMP (inosine monophosphate) dehydrogenase 2 /DB_XREF=gi:4504688 /UG-Hs.75432 IMP (inosine monophosphate) dehydrogenase 2 /FI=gb:U04208.1 gb:NM_000888.1	
217905_at	gb:NM_0246834.1 /DEF=Homo sapiens hypothetical protein FLJ13081 (FLJ13081), mRNA. /FEA=mRNA /GEN=FLJ13081 /PROD=hypothetical protein FLJ13081 /DB_XREF=gi:13376242 /UG-Hs.180638 hypothetical protein FLJ13081 /FI=gb:BC004183.1 gb:NM_0246834.1	
209036_s_at	gb:BC001917.1 /DEF=Homo sapiens malate dehydrogenase 2, NAD (mitochondrial), clone MGC:3559, mRNA, complete cds. /FEA=mRNA /PROD=malate dehydrogenase 2, NAD (mitochondrial) /DB_XREF=gi:12804328 /UG-Hs.111076 malate dehydrogenase 2, NAD (mitochondrial) /FI=gb:BC001917.1 gb:NM_003918.1	

222010_at	Consensus includes qb:BF224073 /FEA=EST /DB_XREF=est:7q83e05.x1 /CLONE=IMAGE·3704936 /UG=Hs.278544 acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
203875_at	qb:NN_00711.2 /DEF=Homo sapiens bromodomain-containing 3 (BRD3), mRNA. /FEA=mRNA /GEN=BRD3 /PROD=bromodomain-containing protein 3 /DB_XREF=gi:12400642 /UG=Hs. 86896 bromodomain-containing 3 /FL=gb:NM_0013711.2 /gb:D26362.1
202943_s_at	qb:NM_038083.1 /DEF=Human alpha-N-acetylgalactosaminidase mRNA, complete cds. /FEA=mRNA /PROD=alpha-N-acetylgalactosaminidase /DB_XREF=gi:189054 /UG=Hs. 75372 N-acetylgalactosaminidase, alpha-/EL=gb:BC000951.5.1 qb:NM_000262.1
210555_s_at	qb:085430.1 /DEF=Human transcription factor NEATX4 mRNA, complete cds. /FEA=mRNA /PROD=transcription factor NEATX4 /DB_XREF=gi:1835590 /UG=Hs. 172674 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 /FL=gb:UB85430.1
218370_s_at	qb:NN_022753.1 /DEF=Homo sapiens hypothetical protein FLJ12903 (FLJ12903), mRNA. /FEA=mRNA /GEN=FLJ12903 /PROD=hypothetical protein FLJ12903 /DB_XREF=gi:12232418 /UG=Hs. 14928 hypothetical protein FLJ12903 /FL=gb:NN_022753.1
208070_s_at	qb:NN_00912.1 /DEF=Homo sapiens REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta (REV3L), mRNA. /FEA=mRNA /GEN=REV3L /PROD=REV3L (yeast homolog)-like, catalytic subunit of DNA polymerase zeta /DB_XREF=gi:4506482 /UG=Hs. 115521 REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta /EL=gb:AF078695.1 qb:NM_002912.1 qb:AF179428.1
201212_at	qb:NM_001628.1 /DEF=Homo sapiens aldo-keto reductase family 1, member B1 (aldose reductase) /AKRIB1, mRNA. /FEA=mRNA /GEN=AKRIB1 /PROD=aldo-keto reductase family 1, member B1 (aldose reductase) /DB_XREF=gi:4502048 /UG=Hs. 75313 aldo-keto reductase family 1, member B1 (aldose reductase) /EL=gb:BC000260.1 qb:J04795.1 qb:NM_001628.1
209824_s_at	qb:AB000812.1 /DEF=Homo sapiens mRNA for BMAL1b, complete cds. /FEA=mRNA /PROD=BMAL1b /DB_XREF=q1:2094734 /UG=Hs. 74515 aryl-hydrocarbon receptor nuclear translocator-like /FL=gb:AB000812.1 qb:AF044286.1
209064_x_at	qb:NM_0136920.1 /DEF=Homo sapiens mRNA; cDNA DK2XP58C051 (from clone DKFZp58C051); complete cds. /FEA=mRNA /GEN=DKFZp58C051 /PROD=hypothetical protein /DB_XREF=gi:12053334 /UG=Hs. 109643 polyadenylate binding protein-interacting protein 1 /FL=gb:AU136920.1
200759_x_at	qb:NM_003204.1 /DEF=Homo sapiens nuclear factor (erythroid-derived 2)-like 1 (NFE2L1), mRNA. /FEA=mRNA /GEN=NFE2L1 /PROD=transcript /PROD=q1:4505378 /UG=Hs. 83469 nuclear factor (erythroid-derived 2)-like 1 /FL=gb:NM_003204.1 qb:NN_001628.1
221707_at	Consensus includes qb:BF431618 /FEA=EST /DB_XREF=gi:11443732 /DB_XREF=est:7616e03.x1 /CLONE=IMAGE·3574349 /UG=Hs. 12342 Homo sapiens clone 24538 mRNA sequence
211561_x_at	qb:AF000426.1 /DEF=Homo sapiens LST1 mRNA, CLSP1E splice variant, complete cds. /FEA=mRNA /GEN=LST1 /DB_XREF=gi:2145067 /UG=Hs. 88411 lymphocyte antigen 117 /FL=gb:AF000426.1
37384_at	Cluster Incl. D13640:Human mRNA for KIAA0015 gene, complete cds /cds=(106,1470) /gb:D13640 /gi:286006 /ug:Hs. 77961 /len=5134
218423_x_at	qb:NM_016516.1 /DEF=Homo sapiens tumor antigen SLP-8p (HCC8), mRNA. /FEA=mRNA /GEN=HCC8 /PROD=tumor antigen SLP-8p /DB_XREF=gi:7705396 /UG=Hs. 48498 tumor antigen SLP-8p /FL=gb:AF102177.1 qb:NM_016516.1
210213_s_at	qb:AF02229.1 /DEF=Homo sapiens translation initiation factor 6 (EIF6), mRNA, complete cds. /FEA=mRNA /GEN=eIF6 /PROD=translation initiation factor 6 /DB_XREF=gi:2809382 /UG=Hs. 5215 interein beta 4 binding protein /EL=gb:AF02229.1
201598_s_at	qb:NM_001567.2 /DEF=Homo sapiens inositol polyphosphate phosphatase-like 1 (INPP1L), mRNA. /FEA=mRNA /GEN=INPP1L /PROD=Inositol polyphosphate phosphatase-like 1 /DB_XREF=gi:4755141 /UG=Hs. 75339 inositol polyphosphate phosphatase-like 1 /FL=gb:NM_001567.2 qb:124444.1
204301_at	qb:NM_014867.1 /DEF=Homo sapiens KIAA0711 gene product (KIAA0711), mRNA. /FEA=mRNA /GEN=KIAA0711 /PROD=KIAA0711 gene product /DB_XREF=gi:7662259 /UG=Hs. 5333 KIAA0711 gene product /FL=gb:AB01854.1 qb:NM_014867.1
202877_s_at	Consensus includes qb:W72082 /FEA=EST /DB_XREF=est:zd70c06.s1 /CLONE=IMAGE·315994 /UG=Hs. 97199 complement component C1q receptor /FL=gb:NM_012012.2 qb:U94333.1
208772_at	qb:NM_01081.1 /DEF=Homo sapiens anaphase-promoting complex subunit 5, clone MGC:2755, mRNA, complete cds. /FEA=mRNA /PROD=anaphase-promoting complex subunit 5 /DB_XREF=gi:12654502 /UG=Hs. 7101 anaphase-promoting complex subunit 5 /EL=gb:BC001081.1 qb:NM_01081.1 qb:AF1333.1 qb:NM_016237.1
201998_at	Consensus includes qb:AF743792 /FEA=EST /DB_XREF=gi:5112080 /DB_XREF=est:wg53h11.x1 /CLONE=IMAGE·2368869 /UG=Rs. 2554 sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) /EL=gb:NM_003032.1
208722_s_at	qb:BC001081.1 /DEF=Homo sapiens anaphase-promoting complex subunit 5, clone MGC:2755, mRNA, complete cds. /FEA=mRNA /PROD=anaphase-promoting complex subunit 5 /DB_XREF=gi:12654502 /UG=Hs. 7101 anaphase-promoting complex subunit 5 /EL=gb:BC001081.1 qb:BC001081.1 qb:AF1333.1 qb:NM_016237.1
55692_at	Cluster Incl. W22924:75H3 Homo sapiens cDNA /clone=(not-directional) /gb:W22924 /gi=1299757 /ug:Hs. 96560 /len=792
217954_s_at	qb:NM_015153.1 /DEF=Homo sapiens KIAA0244 protein (KIAA0244), mRNA. /FEA=mRNA /GEN=KIAA0244 /PROD=KIAA0244 protein /DB_XREF=gi:17662017 /UG=Hs. 78893 KIAA0244 protein /FL=gb:AF091622.1 qb:NM_015153.1

220307_at	gb:NM_016382.1 /DEF=Homo sapiens natural killer cell receptor 2B4 (CD244), mRNA. /FEA=mRNA /GEN=CD244 /PROD=natural killer cell receptor 2B4 /FL=q:AF24240.1 gb:AF105261.1
211989_at	gb:AF101761.2 gb:AC11711.1 gb:NM_016382.1 Consensus includes gb:NM_003079.1 /DEF=Homo sapiens SWISNF related, actin dependent regulator of chromatin, subfamily e, member 1 (SMARCE1), mRNA. /FEA=CDS /GEN=SMARCE1 /PROD-SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 /DB_XREF=q:is_332848 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 /FL=q:NM_003079.1
209303_at	gb:BC005270.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase), mRNA, complete cds. /FEA=mRNA /PROD=NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) /DB_XREF=q:is_10758 NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) /FL=q:BC005270.1 gb:AF020351.1 gb:NM_002495.1
201729_s_at	gb:NM_014660.1 /DEF=Homo sapiens KIAA0100 gene product (KIAA0100), mRNA. /FEA=mRNA /GEN=KIAA0100 /PROD=KIAA0100 gene product /DB_XREF=q:1.7661903 /UG=Hs.151761 KIAA0100 gene product /FL=q:DB_043947.1 gb:NM_014680.1
203330_s_at	gb:NM_004604.1 /DEF=Homo sapiens syntaxis 4A (placental) (STX4A), mRNA. /FEA=mRNA /GEN=STX4A /PROD=syntaxin 4A (placental) /DB_XREF=q:1.4759185 /UG=Hs.83734 syntaxis 4A (placental) /FL=q:BC002436.1 gb:AF026007.1 gb:NM_004604.1
201622_at	gb:NM_014380.1 /DEF=Homo sapiens EBNA-2 co-activator (100kD) (P100), mRNA. /FEA=mRNA /GEN=p100 /PROD=EBNA-2 co-activator (100kD) /DB_XREF=q:1.7657430 /UG=Hs.79093 EBNA-2 co-activator (100kD) /FL=q:NM_014390.1 gb:U22055.1

Tabelle 2: Gene aus Clusteranalyse 2

Affymetrix-interne Bezeichnung	Beschreibung der Sequenz in der GeneBank Datenbank
200654_at	gb:J02283.1 /DEF=Human thyroid hormone binding protein (p55) mRNA, complete cds. /FEA=mRNA /GEN=PAHB /DB_XREF=gi:3339546 /UG-Hs_7565/procollagen-proline, 2-oxoglutamate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein P55) /FL=gb:J02283.1 qb:NM_000918.1
203126_at	gb:NM_014244.1 /DEF=Homo sapiens inositol myo-1 (or 4)-monophosphatase 2 (IMPA2) , mRNA. /FEA=mRNA /GEN=IMPA2 /PRO=Inositol (myo)-1 (or 4)-monophosphatase 2 /DB_XREF=gi:1657235 /UG-Hs_5753 inositol (myo)-1 (or 4)-monophosphatase 2 /EL=gb:AF200432.1qb:NM_014244.1 qb:AF014398.2
203585_at	gb:NM_007150.1 /DEF=Homo sapiens zinc finger protein 185 (ZNF185) , mRNA. /FEA=mRNA /GEN=ZNF185 /PRO=zinc finger protein 185 (ZNF domain) /DB_XREF=gi:1005971 /UG-Hs_16622 zinc finger protein 185 (ZNF domain) /FL=gb:NM_007150.1
205220_at	gb:NM_006018.1 /DEF=Homo sapiens putative chemokine receptor; GTP-binding protein (RMT74) , mRNA. /FEA=mRNA /GEN=RMT74 /PRO=putative chemokine receptor; GTP-binding protein /DB_XREF=gi:5174460 /UG-Hs_137555 putative chemokine receptor; GTP-binding protein /EL=gb:NM_006018.1
207008_at	gb:NM_001557.1 /DEF=Homo sapiens interleukin 8 receptor, beta (IL8RB) , mRNA. /FEA=mRNA /GEN=IL8RB /PRO=interleukin 8 receptor, beta /DB_XREF=gi:4504682 /UG-Hs_846 interleukin 8 receptor, beta /FL=gb:NM4582.1 qb:NM_001557.1 qb:L19593.1
200897_s_at	gb:NM_016081.1 /DEF=Homo sapiens palladin (KIAA0992) , mRNA. /FEA=mRNA /GEN=KIAA0992 /PRO=palladin /UG-Hs_194431 palladin /FL=gb:AF07041.1 qb:AF151909.1 qb:NM_016081.1
205568_at	gb:NM_020980.2 /DEF=Homo sapiens aquaporin 9 (AQP9) , mRNA. /FEA=mRNA /GEN=AQP9 /PRO=aquaporin 9 /DB_XREF=gi:11038652 / gb:NM_0104624 aquaporin 9 /FL=gb:NW_020980.2 qb:AB008775.1 qb:AF016495.1
2114022_s_at	Consensus includes gb:NM_0419101 /FEA=EST /DB_XREF=gi:2789059 /DB_XREF=est:ny11d02.s1 /CLONE=IMAGE:1271427 / gb:NM_146360 interferon induced transmembrane protein 1 (9-27)
209762_x_at	gb:AF280094.1 /DEF=Homo sapiens transcriptional coactivator Sp110B mRNA, complete cds. /FEA=mRNA /PRO=Sp110B mRNA, complete cds. /DB_XREF=gi:3800093 /DB_XREF=gi:3800093 /DB_XREF=gi:3800093 /PRO=uridine phosphorylase
203234_at	gb:NM_003364.1 /DEF=Homo sapiens uridine phosphorylase (UP) , mRNA. /FEA=mRNA /GEN=UP /PRO=uridine phosphorylase /DB_XREF=gi:4507838 /UG-Hs_77573 uridine phosphorylase FL=gb:BC001405.1 qb:NM_003364.1
2011940_at	Consensus includes gb:NM_0499514 /FEA=EST /DB_XREF=gi:3034114 /DB_XREF=est:aj625212.s1 /CLONE=IMAGE:13941879 /UG-Hs_5057 carboxypeptidase D /FL=gb:DP85390.1 qb:D85390.1 qb:NM_011034.2
209310_s_at	gb:NM_025804.1 /DEF=Human Ich-2 cysteine protease mRNA, complete cds. /FEA=mRNA /PRO=Ich-2 /DB_XREF=gi:7886049 /UG-Hs_741122 caspase 4, apoptosis-related cysteine protease /FL=gb:U23976.1 qb:U23977.1 qb:U23978.1 qb:NM_001225.1 qb:U23804.1 qb:U23014.1
202128_at	gb:NM_014821.1 /DEF=Homo sapiens KIAA0317 gene product (KIAA0317) , mRNA. /FEA=mRNA /GEN=KIAA0317 /PRO=KIAA0317 gene product /DB_XREF=gi:7662051 /UG-Hs_20126 KIAA0317 gene product /FL=gb:AB02315.1 qb:NM_014821.1
201192_s_at	gb:NM_006224.1 /DEF=Homo sapiens phosphotidylinositol transfer protein (PTPN) , mRNA. /FEA=mRNA /GEN=PTPN /PRO=phosphotidylinositol transfer protein /DB_XREF=gi:5453907 /UG-Hs_79709 phosphotidylinositol transfer protein /FL=gb:D30036.1 qb:NM_006224.1
208012_x_at	gb:NM_004509.1 /DEF=Homo sapiens interferon-induced protein 41, 30kD (IFI41) , mRNA. /FEA=mRNA /GEN=IFI41 / PRO=interferon-induced protein 41, 30kD /DB_XREF=gi:4758885 /UG-Hs_241510 interferon-induced protein 41, 30kD / EL=gb:122342.1 qb:NM_004509.1
209137_s_at	gb:NC000263.1 /DEF=Homo sapiens, Similar to ubiquitin c-terminal hydrolase related polypeptide, clone MGC:2621, mRNA, complete cds. /FEA=mRNA /PRO=Similar to ubiquitin c-terminal hydrolaserelated polypeptide /DB_XREF=gi:12653004 / gb:Hs_78829 ubiquitin specific protease 10 /FL=gb:BC000263.1
2118023_s_at	gb:NM_016605.1 /DEF=Homo sapiens putative nuclear protein (LOC51307) , mRNA. /FEA=mRNA /GEN=LOC51307 / PRO=putative nuclear protein /DB_XREF=gi:7706138 /UG-Hs_102469 putative nuclear protein /FL=gb:AF251040.1 qb:NM_016605.1
201190_s_at	Consensus includes gb:NM_0179709 /FEA=EST /DB_XREF=gi:8800467 /DB_XREF=est:yM72109.s1 /CLONE=IMAGE:49287 / gb:NM_0179709 phosphotidylinositol transfer protein /FL=gb:J30056.1 qb:M73104.1 qb:NM_006224.1
2110563_x_at	gb:NM_0190705.1 /DEF=Homo sapiens F11C-like inhibitory protein short form /DB_XREF=gi:2253680 /UG-Hs_195175 CASP8 and FADD-like apoptosis regulator /PRO=F11C-like inhibitory protein short form /DB_XREF=gi:2253680 /UG-Hs_195175 CASP8 and FADD-like apoptosis regulator /

	EL=gb:U97075_1	Consensus includes gb:BE788439 / FEA=EST / DB_XREF=gi:10209637 / DB_XREF=est:601475616F1 / CLONE=IMAGE:3878643 / UG=hs.247280 HbV associated factor
221827_at	gb:NM_004214_3 / DEF=Homo sapiens fibroblast growth factor (acidic) intracellular binding protein (FIBP), mRNA / FEA=mRNA / GEN=FIBP / PRO=fibroblast growth factor (acidic) intracellular binding protein / EL=gb:AF171944.1 qb:AF171946.1	
202041_s_at	gb:NM_004214_3 / DEF=Homo sapiens fibroblast growth factor (acidic) intracellular binding protein (FIBP), mRNA / FEA=mRNA / GEN=FIBP / PRO=fibroblast growth factor (acidic) intracellular binding protein / EL=gb:AF171944.1 qb:AF171946.1	
212975_at	gb:NM_07768 Homo sapiens fibroblast growth factor (acidic) intracellular binding protein / EL=gb:AF10187.2 qb:NM_004214.3	
201001_s_at	Consensus includes gb:BG164064 / FEA=EST / DB_XREF=gi:12670767 / DB_XREF=est:6024109F1 / CLONE=IMAGE:4449022 / UG=hs.75875 ubiquitin-conjugating enzyme E2 variant 1 / FL=gb:U39361.1 qb:NM_003349.2 qb:BC0000468.1	
212975_at	Consensus includes gb:AB020677.2 / DEF=Homo sapiens mRNA for KIAA0870 protein, partial cds. / FEA=mRNA / GEN=KIAA0870 / PROD=KIAA0870 protein / DB_XREF=gi:66335136 / UG=hs.18166 KIAA0870 peptide	
201412_at	gb:NM_014045.1 / DEF=Homo sapiens DKZBP564C1940 protein (DKZBP564C1940), mRNA. / FEA=mRNA / GEN=DKEBP564C1940 / PROD=DKEBP564C1940 protein / DB_XREF=gi:13207587 / UG=hs.3804 DKZBP564C1940 protein / FL=gb:BC000424.1 qb:NM_014045.1	
203708_at	gb:NM_002600.1 / DEF=Homo sapiens phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4 (PDE4B) mRNA. / FEA=mRNA / GEN=PDE4B / PROD=phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) / DB_XREF=gi:1505662 / UG=hs.188 phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) / FL=gb:MG97515.1 qb:NM_02600.1	
203907_s_at	gb:NN_01465.1 / DEF=Homo sapiens KIAA0763 gene product (KIAA0763), mRNA. / FEA=mRNA / GEN=KIAA0763 / PROD=KIAA0763 gene product / DB_XREF=gi:71662289 / UG=hs.4764 KIAA0763 gene product / FL=gb:AB018306.1 qb:NM_014869.1	
209882_at	gb:AB084462.1 / DEF=Homo sapiens GTP-binding protein ROC1 (ROC1), mRNA, complete cds. / FEA=mRNA / GEN=ROC1 / PROD=GTP-binding protein ROC1 / DB_XREF=gi:1234917 / UG=hs.96038 RIC (Drosophila)-like, expressed in many tissues / FL=gb:UT1203.1 qb:UT8165.1 qb:AF081462.1 qb:NM_006912.1	
204276_at	Consensus includes gb:BB895437 / DEF=EST / DB_XREF=gi:10358829 / DB_XREF=est:60137912F1 / CLONE=IMAGE:3922971 / UG=hs.274701 thymidine kinase 2, mitochondrial / FL=gb:NM_004614.1 qb:UT7088.1	
221984_s_at	Consensus includes gb:AB040896 / FEA=EST / DB_XREF=gi:5409841 / DB_XREF=est:DKEBP43412415_s1 / CLONE=DKEBP43412415 / UG=hs.22412 hypothetical protein MEC3035	
218517_at	gb:NM_024900.1 / DEF=Homo sapiens hypothetical protein FLJ22479 (FLJ22479), mRNA. / FEA=mRNA / GEN=FLJ22479 / PROD=hypothetical protein FLJ22479 (FLJ22479), mRNA, partial cds. / UG=hs.23246 hypothetical protein FLJ22479 / FL=gb:NM_024900.1	
208740_at	Consensus includes gb:BB591650 / FEA=EST / DB_XREF=gi:11685974 / DB_XREF=est:nacd01.x1 / CLONE=IMAGE:3275957 / UG=hs.23964 sin3-associated polypeptide, 18kD / FL=gb:NM_005870.2 qb:U96915.1 qb:UT8303.1	
221484_at	Consensus includes gb:BB691447 / FEA=EST / DB_XREF=gi:11976055 / DB_XREF=est:602247615F1 / CLONE=IMAGE:43328663 / UG=hs.107526 UDP-Gal:betaGalNAc beta 1,4-galactosyltransferase, polypeptide 5 / FL=gb:AB004550.1 qb:NM_004776.1	
209575_at	gb:NC_001903.1 / DEF=Homo sapiens. Similar to interleukin 10 receptor, beta. Clike MGC:2210. mRNA, complete cds. / FEA=mRNA / PROD=Similar to interleukin 10 receptor, beta / DB_XREF=gi:12804902 / UG=hs.173936 interleukin 10 receptor, beta / FL=gb:BC001903.1 qb:NM_000628.1	
200619_at	gb:NN_006842.1 / DEF=Homo sapiens splicing factor 3b, subunit 2, 145kD / DB_XREF=gi:5803154 / UG=hs.75916 splicing factor 3b, subunit 2, 145kD / FL=gb:U1371.1 qb:NM_006842.1	
217286_s_at	Consensus includes gb:BG001805.1 / DEF=Homo sapiens, clone IMAGE:3543670, mRNA, partial cds. / FEA=mRNA / PROD=Unknown (protein for IMAGE:3543670) / DB_XREF=gi:12804742 / UG=hs.240615 hypothetical protein FLJ13556 similar to N-myristoylstream regulated 3	
207842_s_at	gb:NM_007355.1 / DEF=Homo sapiens MN51 protein (MN51), mRNA. / FEA=mRNA / GEN=MN51 / PROD=MN51 protein / DB_XREF=gi:6676887 / UG=hs.83422 MN51 protein	
217788_s_at	gb:NM_004481..2 / DEF=Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) (GAINT2), mRNA. / FEA=mRNA / GEN=GAINT2 / PROD=polypeptide N-acetylgalactosaminyltransferase 2 / DB_XREF=gi:9945385 / UG=hs.130181 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) / FL=gb:NM_004481.2	
48612_at	Cluster Incl. AA225490-nc25b01.r1 Homo sapiens cDNA / clone=IMAGE-1009129 / gb:AA225490 / gi=1846817 / ug=Hs.80115 / len=539	
212669_s_at	Consensus includes gb:BA52505 / FEA=EST / DB_XREF=gi:2265433 / CLONE=IMAGE:ng43g12.s1 / UG=hs.321707 KIAA0142 protein	

222047_s_at	Consensus includes gb:AI523895 /FEA=EST /DB_XREF=gi:4438030 /DB_XREF=est:tg97g03.x1 /CLONE=IMAGE:21116756 /
201666_at	gb:NM_003254.1 /DEF=Homo sapiens tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMPI), mRNA. /FEA=mRNA /GEN=TIMP1 /PROD=tissue inhibitor of metalloproteinase 1precursor /
	DB_XREF=gi:45071508 /UG-Hs_5831 tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) /FL=gb:BC000866.1 qb:NM_003254.1
203218_at	Consensus includes gb:W7431 /FEA=EST /DB_XREF=est:gi:1319025 /DB_XREF=est:xc11f1.1.s1 /CLONE=IMAGE:322029 /
	Ue-Hs_246857 nitrogen-activated protein kinase 9 /FL=qb:U34821.1 qb:NM_002752.1 qb:L31951.1 qb:009759.1
213118_at	Consensus includes gb:AI336821.1 /DEF=Homo sapiens mRNA; cDNA DKFZp34M1526 (from Clone DKFZp43M1526) . /FEA=mRNA /
	GRN=DKEZp34M1526 /PROD=hypothetical protein /DB_XREF=gi:12053152 /UC=Hs_1525293 KIA0701 protein
201057_s_at	gb:NM_004487.1 /DEF=Homo sapiens golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 (GOLGB1), mRNA. /FEA=mRNA /GRN=GOLGB1 /PROD=golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 /
208648_at	DB_XREF=gi:4758453 /UG-Hs_7844 golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 /
212242_at	FI=qb:NM_004487.1
217738_at	Consensus includes gb:BF375514 /FEA=EST /DB_XREF=gi:11649318 /DB_XREF=est:602133090FL /CLONE=IMAGE:4288079 /
	Ue-Hs_239138 pre-B-cell colony-enhancing factor /FL=qb:U02020.1 qb:NM_005746.1
203897_at	Consensus includes gb:W60953 /FEA=EST /DB_XREF=est:gi:1367731 /DB_XREF=est:ac98012.s1 /CLONE=IMAGE:339167 /
	Ue-Hs_106357 valosin-containing protein /FL=qb:AF100752.1 qb:NM_007126.2
	Consensus includes gb:AL556074 /FEA=EST /DB_XREF=est:gi:12916087 /DB_XREF=est:AU565074 /CLONE=CS0DN0031F20 (3 prime) /
	Ue-Hs_75318 tubulin, alpha 1 (testis specific)
203897_at	Consensus includes gb:BE963444 /FEA=EST /DB_XREF=gi:11766863 /DB_XREF=est:601657224RI /CLONE=IMAGE:3866357 /
	gb:NM_020424.1
209513_s_at	gb:BC004331.1 /DEF=Homo sapiens similar to RIKEN cDNA 2610207116 gene, clone MGC:10940, mRNA, complete cds. /
	Similar to RIKEN cDNA 2610207116 gene, clone MGC:10940, mRNA, complete cds /FL=qb:BC004331.1
211762_s_at	gb:BC05978.1 /DEF=Homo sapiens, karyopherin alpha 2 (RAG cohort 1, importin alpha 1), clone MGC:11668, mRNA, complete cds. /
	FEA=mRNA /PROD=karyopherin alpha 2 (RAG cohort 1, importin alpha 1), DB_XREF=gi:13543656 /EL=qb:BC005978.1
219639_X_at	gb:NM_0020213.1 /DEF=Homo sapiens hypothetical protein from EUROIMAGE 1977056 (LOC56965), mRNA. /FEA=mRNA /
	GEN=LOC56965 /PROD=hypothetical protein from EUROIMAGE 1977056 /DB_XREF=gi:9910373 /UG=us_315687 hypothetical protein from EUROIMAGE 1977056 /FI=qb:NM_0020213.1
217882_at	gb:NM_018447.1 /DEF=Homo sapiens 30 kDa protein (LOC55831), mRNA. /FEA=mRNA /GEN=LOC55831 /PROD=30 kDa protein /
	DB_XREF=gi:8223856 /UG-Hs_283714 30 kDa protein /FL=qb:AF157321.1 qb:NM_018047.1
204714_s_at	gb:NM_000130.2 /DEF=Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5), mRNA. /FEA=mRNA /GEN=F5 /
	PROD=coagulation factor V precursor /DB_XREF=gi:10518500 /UG-Hs_3054 coagulation factor V (proaccelerin, labile factor) /
221547_at	gb:BC000794.1 /DEF=Homo sapiens, pre-mRNA splicing factor similar to S. cerevisiae Prp18, clone MGC:5075, mRNA, complete cds. /FEA=mRNA /PROD=pre-mRNA splicing factor similar to S.cerevisiae Prp18 /DB_XREF=gi:12653992 /
	Ue-Hs_155244 pre-mRNA processing factor 18 /FL=qb:BC000794.1 qb:NM_003675.1
210793_s_at	gb:U1815.1 /DEF=Human nucleoporin 98 (NUF98), mRNA, complete cds. /FEA=mRNA /GEN=NUF98 /PROD=nucleoporin 98 /
	DB_XREF=gi:1184172 /UG-Hs_112255 nucleoporin 98kd /FI=qb:U41815.1
206207_at	gb:NM_001828.3 /DEF=Homo sapiens Charot-Leyden crystal protein (CLC), mRNA. /FEA=mRNA /GEN=CLC /
	PROD=Charot-Leyden crystal protein /DB_XREF=gi:6325164 /UG-Hs_889 Charot-Leyden crystal protein /
	FI=qb:J01664.1 qb:NM_001828.3
202595_s_at	gb:AF161461.1 /DEF=Homo sapiens HSPC112 mRNA, complete cds. /FEA=mRNA /PROD=HSPC112 /DB_XREF=gi:6841445 /
	Ue-Hs_11000 leptin receptor overlapping transcript-like 1 /FL=qb:BC000642.1 qb:AF053605.1 qb:AF16161.1 qb:NM_015344.1
219434_at	gb:NM_018643.1 /DEF=Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), mRNA. /FEA=mRNA /GEN=TREMI /
	PROD=triggering receptor expressed on myeloid cells 1 /FL=qb:AF196329.1 qb:NM_018643.1 qb:AF27008.1
205020_s_at	gb:NM_005738.1 /DEF=Homo sapiens ADP-ribosylation factor-like 4 (ARF4), mRNA. /FEA=mRNA /GEN=ARF4 /
	PROD=ADP-ribosylation factor-like 4 /DB_XREF=gi:5031602 /UG-Hs_201672 ADP-ribosylation factor-like 4 /
212052_s_at	gb:U73960.1 qb:NM_005738.1
	Consensus includes gb:AB014576.1 /DEF=Homo sapiens mRNA for KIAA0676 protein, partial cds. /FEA=mRNA /
	GEN=KIAA0676 /PROD=KIAA0676 protein /DB_XREF=gi:13327165 /UG-Hs_155829 KIAA0676 protein

202565_s_at	gb:NM_003174.2 / DEF=Homo sapiens super villin (SVIL), transcript variant 1, mRNA. /FEA=mRNA /GEN=SVIL /PROD=supervillin isoform 1 /DB_XREF=gi:11496980 /UG=Hs_154567 supervillin /EL=gb:NM_003174.2 qb:AF051851.1
221524_s_at	gb:AF27036.1 /DEF=Homo sapiens Rag D mRNA, complete cds /DB_XREF=gi:11181619 /
221525_s_at	gb:HS_238679 Rag D protein /EL=gb:NM_021244.1 qb:AF272036.1 qb:BC003088.1
218037_at	gb:NM_024293.1 /DEF=Homo sapiens hypothetical protein MGC3035 (MGC3035), mRNA. /FEA=mRNA /GEN=MGC3035 /PROD=hypothetical protein MGC3035 /DB_XREF=gi:11323551 /UG=Hs_22412 hypothetical protein MGC3035 /EL=gb:ALL136756.1 qb:NM_024293.1
214107_x_at	Consensus includes gb:AW310850 /FEA=EST /DB_XREF=gi:6837476 /DB_XREF=est:xs31f01.x1 /CLONE-IMAGE:2761753 /UG=Hs_3266350 Homo sapiens cDNA FLJ11822 fis, clone HEMB1006485, highly similar to PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.1.11.-)
210184_at	gb:MB81695.1 /DEF=H.sapiens leukocyte adhesion glycoprotein P150,95 mRNA, complete cds. /FEA=mRNA /GEN=ITGAX /DB_XREF=gi:487829 /DG=Hs_51077 integrin, alpha X (lantigen CD11C (p150), alpha Polypept.de) /EL=gb:NM_0008887.2
209107_x_at	gb:U19179.1 /DEF=Human (Hun-2) mRNA, complete cds. /FEA=mRNA /GEN=Hin-2 /DB_XREF=gi:726037 /
208749_x_at	gb:AF085357.1 /DEF=Homo sapiens receptor activator 1 /EL=gb:U19179.1
215561_at	Consensus includes gb:AA319595 /FEA=EST /DB_XREF=gi:2001934 /DB_XREF=est:EST15629 /UG=Hs_26197 KIAA1091 protein
212470_at	Consensus includes gb:AB011088.1 /DEF=Homo sapiens mRNA for KIAA0516 protein, partial cds. /FEA=mRNA /GEN=KIAA0516 /PROD=KIAA0516 protein /DB_XREF=gi:304555 /UG=Hs_129872 sperm associated antigen 9
2114937_x_at	Consensus includes gb:AI924817 /FEA=EST /DB_XREF=gi:15660781 /DB_XREF=est:wn23c11.x1 /CLONE-IMAGE:2446232 /UG=Hs_75737 paracentriolar material 1
2021783_s_at	gb:NM_021975.1 /DEF=Homo sapiens kappa light polypeptide gene enhancer in B-cells 3 (p65) /RELA /PROD=rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in avian reticuloendotheliosis virus) viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) /DB_XREF=gi:11496238 /UG=Hs_75569 v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) /EL=gb:NM_021188.1 /DEF=Homo sapiens clones 23667 and 23775 zinc finger protein [LOC(862)], mRNA. /FEA=mRNA /GEN=LOC51862 /PROD=clones 23667 and 23775 zinc finger protein /DB_XREF=gi:10863934 /UG=Hs_7137 clones 23667 and 23775 zinc finger protein /EL=gb:NM_021188.1 qb:U90919.1
202010_s_at	gb:NM_003641.1 /DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA. /FEA=mRNA /GEN=IFITM1 /PROD=interferon induced transmembrane protein 1 (9-27) /DB_XREF=gi:4504580 /UG=Hs_146360 interferon induced transmembrane protein 1 (9-27) /EL=gb:NM_021030.1 qb:U17743.1
201601_x_at	gb:NM_003641.1 /DEF=Homo sapiens mitogen-activated protein kinase 4 (MAP2K1), mRNA. /FEA=mRNA /GEN=MAP2K4 /PROD=mitogen-activated protein kinase 4 /DB_XREF=gi:4506888 /UG=Hs_75217 nitrogen-activated protein kinase 4 /EL=gb:NM_003641.1 qb:U17743.1
2023266_s_at	gb:NM_003010.1 /DEF=homo sapiens cyclin-E binding protein 1 (LOC51191), mRNA. /FEA=mRNA /GEN=LOC51191 /PROD=cyclin-E binding protein 1 /DB_XREF=gi:70705930 /UG=Hs_26663 cyclin-E binding protein 1 /EL=gb:AB027289.1 qb:NM_016323.1
21219863_at	Consensus includes gb:BE999972 /FEA=EST /DB_XREF=gi:10700248 /DB_XREF=est:7h15b02.x1 /CLONE-IMAGE:3316011 /UG=Hs_186613 sphingomyelin-1-phosphate lyase 1 /EL=gb:AF144638.1
21213222_at	gb:NM_020310.1 /DEF=homo sapiens MAX binding protein (MNT), mRNA. /FEA=mRNA /GEN=MNT /PROD=MAX binding protein /DB_XREF=gi:9345317 /UG=Hs_25197 MAX binding protein /EL=gb:NM_020310.1
2020206_at	gb:NM_016621.1 /DEF=homo sapiens hypothetical protein (LOC51317), mRNA. /FEA=mRNA /GEN=LOC51317 /PROD=hypothetical protein /DB_XREF=gi:7706819 /UG=Hs_106816 KIAA1696 protein /EL=gb:NM_016621.1
2023278_s_at	gb:NM_016621.1 /DEF=homo sapiens KIAA0001 gene product; putative G-protein coupled receptor; G protein coupled receptor; G protein coupled receptor for UDP-glucose /DB_XREF=gi:7661847 /UG=Hs_2465 KIAA0001 gene product; putative G-protein coupled receptor; G protein coupled receptor for UDP-glucose /EL=gb:NM_016621.1 qb:NM_014879.1 /DEF=homo sapiens KIAA0001 /PROD=KIAA0001 gene product; putative G-protein coupled receptor; G protein coupled receptor; G protein coupled receptor for UDP-glucose /EL=gb:NM_004388.1 /DEF=mRNA /GEN=CTBS /PROD=chitobiase, di-N-acetyl-beta-D-glucosaminidase /DB_XREF=gi:4758091 /UG=Hs_135578 chitobiase, di-N-acetyl-beta-D-glucosaminidase /EL=gb:NM_004388.1
2020637_at	gb:NM_014879.1 /DEF=homo sapiens KIAA0001 /PROD=KIAA0001 gene product; putative G-protein coupled receptor; G protein coupled receptor; G protein coupled receptor for UDP-glucose /EL=gb:NM_004388.1 /DEF=mRNA /GEN=CTBS /PROD=chitobiase, di-N-acetyl-beta-D-glucosaminidase /DB_XREF=gi:4758091 /UG=Hs_135578 chitobiase, di-N-acetyl-beta-D-glucosaminidase /EL=gb:NM_004388.1
21218924_s_at	gb:NM_004388.1 /DEF=homo sapiens chitobiase, di-N-acetyl-beta-D-glucosaminidase /DB_XREF=gi:4758091 /UG=Hs_135578 chitobiase, di-N-acetyl-beta-D-glucosaminidase /EL=gb:NM_004388.1

Tabelle 3: Gene aus Clusteranalyse 3

Affymetrix-Beschreibung der Sequenz in der GeneBank Datenbank	interne Bezeichnung
Cluster Incl. AI021977-bK44TC4_1 (novel MAF-musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F)	36711_at
Cluster Incl. /cds=(0..494) /gb=AL021977 /gi=914526 /ug=hs.51305 /len=2128	210815_s_at
gb:U08839.1 /DEF=Human urokinase-type plasminogen activator receptor mRNA, complete cds. /FEA=mRNA /PROD=urokinase-type plasminogen activator receptor /EL=gb:U08839.1	202663_s_at
Consensus includes gb:JAI730896 /DB_XREF=gi:179657 plasminogen activator, urokinase receptor /EL=gb:U08839.1 tumor necrosis factor, alpha-induced protein 3 /DB_XREF=gi:5100877 /DB_XREFest:v122602_x1 /CLONE=TMAGE2391026 /UG-Hs.211600 tumor	205476_at
gb:NM_004591.1 /DEF=Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 20 (SCYA20), mRNA. /FEA=mRNA /GEN=SCYA20 /DB_XREF=gi:594651_gb:NM_006290.1	205419_at
gb:NM_004591.1 /DEF=Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 20 (SCYA20), mRNA. /FEA=mRNA /GEN=SCYA20 /DB_XREF=gi:594651_gb:NM_006290.1	209755_at
gb:NM_004591.1 /DEF=Homo sapiens Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) /DB_XREF=gi:1826705 /UG-Hs.784 Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) /EL=gb:108177.1_gb:NM_004951.1	205757_at
gb:NM_004591.1 /DEF=Homo sapiens early activation antigen CD69 mRNA, complete cds. /FEA=mRNA /PROD=early activation antigen CD69 /DB_XREF=gi:291897 /UG-Hs.82401 CD69 antigen (p60, early T-cell activation antigen) /EL=gb:L07555.1_gb:NM_001781.1	203851_at
gb:NM_001432.1 /DEF=Homo sapiens epiregulin /EL=gb:D30783.1_gb:NM_001432.1	211944_s_at
gb:NM_001945.1 /DEF=Homo sapiens diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA. /FEA=mRNA /GEN=DTR /DB_XREF=gi:4503412 /UG-Hs.799 diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) /DB_XREF=gi:4503412 /UG-Hs.799 diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) /EL=gb:M60278.1_gb:NM_001945.1	205403_at
gb:AY029180.1 /DEF=Homo sapiens soluble urokinase plasminogen activator receptor precursor (SUPAR) mRNA, complete cds. /FEA=CDS /GEN=SUPAR /PROD=soluble urokinase plasminogen activator precursor /DB_XREF=gi:131641308 /EL=gb:A1029180.1	206115_at
gb:NM_004633.1 /DEF=Homo sapiens interleukin 1 receptor, type I (IL1R2), mRNA. /FEA=mRNA /GEN=IL1R2 /PROD=interleukin 1 receptor, type II /DB_XREF=gi:4758597 /UG-Hs.25333 interleukin 1 receptor, type II /EL=gb:U74639.1_gb:NM_004633.1	204103_at
gb:NM_005980.1 /DEF=Homo sapiens S100 calcium-binding protein P (S100P), mRNA. /FEA=mRNA /GEN=S100P /PROD=S100 calcium-binding protein P /EL=gb:NM_005980.1	204311_at
gb:NM_004430.1 /DEF=Homo sapiens early growth response 3 (EGFR), mRNA. /FEA=mRNA /GEN=EGFR3 /PROD=early growth response 3 /DB_XREF=gi:4756251 /UG-Hs.74088 early growth response 3 /EL=gb:NM_004430.1	202147_s_at
gb:NM_002984.1 /DEF=Homo sapiens small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA. /FEA=mRNA /GEN=SCYA4 /PROD=small inducible cytokine A4 (homologous to mouse Mip-1b) /DB_XREF=gi:15066944 /UG-Hs.75703 small inducible cytokine A4 (homologous to mouse Mip-1b) /EL=gb:NM_002984.1_gb:NM_002984.1_gb:M25316.1	206522_at
gb:NM_004668.1 /DEF=Homo sapiens maltose-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /FEA=mRNA /GEN=MGAM /PROD=alpha-glucosidase /DB_XREF=gi:4758711 /UG-Hs.122785 maltose-glucoamylase (alpha-glucosidase) /EL=gb:AF016833.1_gb:NM_004668.1	206515_at
gb:NM_001550.1 /DEF=Homo sapiens interferon-related developmental regulator 1 (IERD1), mRNA. /FEA=mRNA /GEN=IERD1 /PROD=Interferon-related developmental regulator 1 /DB_XREF=gi:4504606 /UG-Hs.7879 interferon-related developmental regulator 1 /EL=gb:BC001272.1_gb:NM_001550.1	204614_at
gb:NM_000836.1 /DEF=Homo sapiens cytochrome P450, subfamily IVF, polypeptide 3 (Leukotriene B4 omega hydroxylase) (CYP4F3), mRNA. /FEA=mRNA /GEN=CYP4F3 /PROD=cytochrome P450, subfamily IVF, polypeptide 3 /DB_XREF=gi:4503240 /UG-Hs.106242 cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) /EL=gb:AB024541.1_gb:D12620.1_gb:NM_000836.1	
gb:NM_002575.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 (SERPINB2), mRNA. /FEA=mRNA /GEN=SERPINB2 /PROD=serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 /DB_XREF=gi:4505594 /	

Ug=Hs.75716 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 /EL=gb:J07685.1 qb:NM 002575.1	gb:MI 8082.1
gb:012767_1 /DEF-Human mitogen induced nuclear orphan receptor (MINOR) mRNA, complete cds. /FEA=mRNA /GEN=MINOR /PROD=mitogen induced nuclear orphan receptor /DB_XREF=gi:924281 /UG=Hs.80561 nuclear receptor subfamily 4, group A, member 3 /EL=gb:U12.67.1	
Consensus includes gb:AL050388.1 /DEF=Homo sapiens mRNA; CDNA DKFZP56M2422 (from clone DKFZP56M2422); partial cds /FEA=mRNA /GEN=DKFZP56M2422 /PROD=hypothetical protein /DB_XREF=gi:4914612 /UG=Hs.306320 Homo sapiens mRNA; cDNA DKFZP56M2422 (from clone DKFZP56M2422); partial cds	
Consensus includes qb:BP966236 /FEA=EST /DB_XREF=gi:1171437 /DB_XREF=est:601660172R1 /CLONE=IMAGE:3905920 /UG=Hs.75319 ribonuclease M2 polypeptide /EL=gb:NM 001034.1	
gb:BC05020.1 /DEF=Homo sapiens, peptidylprolyl isomerase F (cyclophilin F), clone MG:11022, mRNA, complete cds. /FEA=mRNA /PROD=peptidylprolyl isomerase F (cyclophilin F) /DB_XREF=gi:1347126 /UG=Hs.173125 peptidylprolyl isomerase F (cyclophilin F) /EL=gb:BC05020.1 qb:NM8054.1 qb:NM 005729.1	
gb:NM_000361.1 /DEF=Homo sapiens thrombomodulin (TBBD), mRNA. /FEA=mRNA /GEN=TBBD /PROD=thrombomodulin /DB_XREF=gi:4507482 /UG=Hs.2030 thrombomodulin /EL=gb:MI6552.1 qb:NM 000361.1	
gb:NM_014059.1 /DEF=Homo sapiens RGC32, mRNA. /FEA=mRNA /GEN=RGC32 /PROD=RGC32 protein /DB_XREF=gi:7662650 /UG=Hs.76640 RGC32 protein /EL=gb:AF036549.1 qb:NM 014059.1	
gb:NM_000519.2 /DEF=Homo sapiens hemoglobin, delta (HBD), mRNA. /FEA=mRNA /GEN=HBD /PROD=hemoglobin, delta /DB_XREF=gi:6633803 /UG=Hs.36977 hemoglobin, delta /EL=gb:NM 000519.2	
gb:NM_002658.1 /DEF=Homo sapiens plasminogen activator, urokinase (PLAU), mRNA. /FEA=mRNA /GEN=PLAU /PROD=plasminogen activator, urokinase /DB_XREF=gi:450582 /UG=Hs.77274 plasminogen activator, urokinase /EL=gb:NM15476.1 qb:NM 002658.1.	
gb:NM_001124.1 /DEF=Homo sapiens adrenomedullin (ADM), mRNA. /FEA=mRNA /GEN=ADM /PROD=adrenomedullin /DB_XREF=gi:4501944 /UG=Hs.394 adrenomedullin /EL=gb:NM 001124.1 qb:DI4874.1	
gb:AF087847.1 /DEF=Homo sapiens GABAR-associated protein like 1 (GABAR1), mRNA, complete cds. /FEA=mRNA /GEN=GABAR1 /PROD=GABA-A receptor-associated protein like 1 /DB_XREF=gi:13315570 /UG=Hs.282654 Homo sapiens mRNA; CDNA DKFZP56M41272 (from clone DKFZP56M41272); complete cds /EL=gb:AI36616.1 qb:AF087847.1	
gb:NM_005569.2 /DEF=Homo sapiens LIN domain kinase 2 (LIMK2), transcrit variant 2a, mRNA. /FEA=mRNA /GEN=LIMK2 /PROD=LIM domain kinase 2 isoform 2a /DB_XREF=gi:8051619 /DB_XREF=gi:8051619 /UG=Hs.278027 LIM domain kinase 2 /EL=gb:DA45906.1 qb:NM 005569.2	
Consensus includes qb:AF070569.1 /DEF=Homo sapiens clone 24659 mRNA sequence. /FEA=mRNA /DB_XREF=gi:1387938 /UG=Hs.23206 Homo sapiens clone 24659 mRNA sequence	
38037_at Cluster Incl. M60278:Human heparin-binding EGF-like growth factor mRNA, complete cds /cds:(261,887) /gb=M60278 /gi=1938666 /Ug=Hs.799 /len=2342	
212723_at Consensus includes qb:AK021780.1 /DEF=Homo sapiens cDNA FUJ11718 fis, clone HEMBA005252, highly similar to Homo sapiens mRNA for KIA040585 protein. /FEA=mRNA /DB_XREF=gi:10433034 /UG=Hs.72660 phosphatidylserine receptor	
207802_at gb:NM_006061.1 /DEF=Homo sapiens specific granule protein (28 kDa); cysteine-rich secretory protein-3 /DB_XREF=gi:5174674 /UG=Hs.54431 specific granule protein (28 kDa); cysteine-rich secretory protein-3 /EL=gb:NM 00661.1	
209967_s_at gb:DI4876.1 /DEF=Human mRNA for hCREM (cyclic AMP-responsive element modulator) type 2 protein, complete cds. /FEA=mRNA /GEN=hCREM-2; hCREM-2; hCREM-2 /PROD=hCREM 2beta-a protein; hCREM 2beta-b protein; hCREM 2alpha-b protein; hCREM 2alpha-a protein /DB_XREF=gi:532036 /UG=Hs.155924 cAMP responsive element modulator /EL=gb:AF069065.1 qb:DI4876.1	
210119_at qb:D73131.1 /DEF=Human inward rectifier potassium channel (Kir1.3), complete cds. /FEA=mRNA /GEN=Kir1.3 /PROD=inward rectifier potassium channel /DB_XREF=gi:1765984 /UG=Hs.17287 potassium inward-rectifying channel, member 15 /EL=gb:U73190.1 qb:NM_002243.1	
203435_s_at qb:NM_007287.1 /DEF=Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CPLA, CD10) (NME), transcript variant 1b1, mRNA. /FEA=mRNA /PROD=membrane metallo-endopeptidase /DB_XREF=gi:6042199 /UG=Hs.1298 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CPLA, CD10) /EL=gb:J03779.1 qb:NM 001287.1 qb:NM 007288.1	
213515_x_at Consensus includes qb:AI133353 /FEA=EST /DB_XREF=gi:16360669 /DB_XREF=est:HA1957 /UG=Hs.298161 myosin, light polypeptide 4, alkali; atrial, embryonic	
209545_s_at qb:AF064824.1 /DEF=Homo sapiens CARD-containing ICE associated kinase mRNA, complete cds. /FEA=mRNA /PROD=CARD-containing ICE associated kinase /DB_XREF=gi:3290171 /UG=Hs.103755 receptor-interacting serine-threonine kinase 2 /EL=gb:BC004553.1	
gb:AF027706.1 qb:AF64824.1 qb:AF078530.1 qb:NM_003821.1	
Consensus includes qb:NM_005566.1 /DEF=Homo sapiens lipocalin 2 (oncogene 24p3) (LCN2), mRNA. /FEA=CDS /GEN=LCN2 /PROD=lipocalin 2 (oncogene 24p3) /DB_XREF=gi:5031852 /UG=Hs.204238 lipocalin 2 (oncogene 24p3) /EL=gb:NM 005564.1	

208470_s_at	gb:NM_020995.1 /DEF=Homo sapiens haptoglobin-related protein (HPR), mRNA. /FEA=CDS /GEN=HPR /PROD=haptoglobin-related protein /DB_XREF=gi:1033758 /EL=gb:NM_020955.1
200733_s_at	gb:U48296.1 /DEF=Homo sapiens Protein tyrosine phosphatase PTPCAAX1 /PROD=protein tyrosine phosphatase PTPCAAX1 /DB_XREF=gi:1777754 /UG=Hs.227777 protein tyrosine phosphatase type IVA, member 1 /EL=gb:U48296.1 gb:NM_003463.1
211372_s_at	gb:U61094.1 /DEF=Human soluble type II interleukin-1 receptor mRNA, complete cds. /FEA=mRNA /PROD=soluble type II Interleukin-1 receptor /DB_XREF=gi:1488065 /UG=Hs.25333 interleukin 1 receptor, type II /EL=gb:U61094.1
204794_at	gb:NM_004118.2 /DEF=Homo sapiens dual specificity phosphatase 2 (DUSP2), mRNA. /FEA=mRNA /GEN=DUSP2 /PROD=dual specificity phosphatase 2 /DB_XREF=gi:12707563 /UG=Hs.1183 dual specificity phosphatase 2 /EL=gb:NM_004118.2 gb:U11329.1
206177_s_at	gb:NM_000457.2 /DEF=Homo sapiens arginase liver (ARGI), mRNA. /FEA=mRNA /PROD=arginase, type I /DB_XREF=gi:10947138 /UG=Hs.289057 arginase liver /EL=gb:NM_000457.2 gb:MI4502.1
205239_at	gb:NM_001657.1 /DEF=Homo sapiens amphiregulin (schwannoma-derived growth factor) (ARGF), mRNA. /FEA=mRNA /GEN=ARGF /PROD=amphiregulin (schwannoma-derived growth factor) /DB_XREF=gi:14502198 /UG=Hs.270833 amphiregulin (schwannoma-derived growth factor) /EL=gb:NM_001657.1
207094_at	gb:NM_000634.1 /DEF=Homo sapiens interleukin 8 receptor, alpha (IL8RA), mRNA. /FEA=mRNA /GEN=IL8RA /PROD=interleukin 8 receptor, alpha /DB_XREF=gi:4504680 /UG=Hs.194778 interleukin 8 receptor, alpha /EL=gb:M68332.1 gb:NM_000634.1 gb:U119551.1
200776_s_at	Consensus includes gb:AL518328 /PROD=EST /DB_XREF=gi:12781821 /DB_XREF=est:AL518328 /CLONE=CSODA09YK18 (3 prime) /UG=Hs.155291
215005_s_at	KLAA0005 gene product /EL=gb:D13620.1 gb:NM_014670.1
215010_s_at	Consensus includes gb:U92014.1 /DEF=Human clone 121711 defective mariner transposon Ksmar2 mRNA sequence. /FEA=mRNA /DB_XREF=gi:1202456 /UG=Hs.153327 Homo sapiens ptn5 mariner-like transposon mRNA, partial sequence
211302_s_at	gb:120966.1 /DEF=Human phosphodiesterase mRNA, complete cds. /FEA=mRNA /PROD=phosphodiesterase /DB_XREF=gi:347121 /UG=Hs.188 phosphodiesterase 4B, cAMP-specific (ducre (Drosophila)-homolog phosphodiesterase E4) /EL=gb:L20966.1
210512_s_at	gb:AF022357.1 /DEF=Homo sapiens vascular endothelial growth factor mRNA, complete cds. /FEA=mRNA /PROD=vascular endothelial growth factor /DB_XREF=gi:371920 /UG=Hs.73793 vascular endothelial growth factor /EL=gb:AF022357.1
212557_at	Consensus includes gb:AA868754 /PROD=EST /DB_XREF=gi:1461199 /DB_XREF=est:ak52e09.s1 /CLONE=IMAGE:1409608
214866_at	Consensus includes gb:X74039.1 /DEF=H. sapiens mRNA for urokinase Plasminogen activator receptor /FEA=mRNA /PROD=urokinase plasminogen activator receptor /DB_XREF=gi:456192 /UG=Hs.179657 plasminogen activator, urokinase receptor
219228_at	gb:NM_018655.2 /DEF=Homo sapiens C2H2-like zinc finger protein (ZNF361), mRNA. /FEA=mRNA /GEN=ZNF361 /PROD=c2H2-like zinc finger protein /DB_XREF=gi:10092612 /UG=Hs.147644 zinc finger protein 331 /EL=gb:AF251515.2 gb:NM_018655.2 gb:AF221248.1
201574_at	gb:NM_004130.1 /DEF=Homo sapiens eukaryotic translation termination factor 1 (ETFL), mRNA. /FEA=mRNA /GEN=ETFL /PROD=eukaryotic translation termination factor 1 /DB_XREF=gi:4759033 /UG=Hs.77324 eukaryotic translation termination factor 1 /EL=gb:U90176.1 gb:NM_004130.1
209498_at	Consensus includes gb:XI6354.1 /DEF=Human mRNA for transmembrane carcinembryonic antigen BCFA (formerly M1-CEA). /FEA=mRNA /PROD=TM1-CEA preprotein /DB_XREF=gi:37197 /UG=Hs.50964 carcinembryonic antigen-related cell adhesion molecule 1 (bilberry glycoprotein) /EL=gb:J03858.1
207630_s_at	gb:NM_001881.1 /DEF=Homo sapiens cAMP responsive element modulator (CREM), mRNA. /FEA=mRNA /GEN=CREM /PROD=cAMP responsive element modulator /DB_XREF=gi:14503038 /UG=Hs.155924 cAMP responsive element modulator /EL=gb:NM_001881.1 gb:S68271.1
210873_x_at	gb:U03891.2 /DEF=Homo sapiens phorbolin I mRNA, complete cds. /FEA=mRNA /PROD=phorbolin I /DB_XREF=gi:1895107 /UG=Hs.226307
204419_x_at	gb:NM_000184.1 /DEF=Homo sapiens hemoglobin, gamma G (HBG2), mRNA. /FEA=mRNA /GEN=HBGG2 /PROD=hemoglobin, gamma G /DB_XREF=gi:6715606 /UG=Hs.283108 hemoglobin, gamma G /EL=gb:NM_000184.1
202988_s_at	gb:NM_002222.1 /DEF=Homo sapiens regulator of G-protein signalling 1 (RGS1), mRNA. /FEA=mRNA /GEN=RGS1 /PROD=regulator of G-protein signalling 1 /DB_XREF=gi:4506534 /UG=Hs.7556 regulator of G-protein signalling 1 /EL=gb:NM_002922.1
208273_s_at	Consensus includes gb:BG8B7555 /PROD=EST /DB_XREF=gi:113261001 /DB_XREF=est:602412371EL1 /CLONE=IMAGE:4521017 /UG=Hs.177776
202693_s_at	Consensus includes gb:AV194730 /PROD=EST /DB_XREF=gi:64747630 /DB_XREF=est:xn43d11.x1 /CLONE=IMAGE:2696469 /UG=Hs.9075
205270_s_at	gb:NM_005665.2 /DEF=Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kd) (LCP2), mRNA. /FEA=mRNA /GEN=LCP2 /PROD=lymphocyte cytosolic protein 2 /DB_XREF=gi:17382491 /UG=Hs.2488 lymphocyte cytosolic protein 2 (LCP2), mRNA. (SH2 domain-containing leukocyte protein of 76kd) /EL=gb:NM_005665.2 gb:U20158.1

202284_s_at	gb:NW_000389.1 /DEF=Homo sapiens cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), mRNA. /FEA=mRNA /GEN=CDKN1A /PROD=cyclin-dependent kinase inhibitor 1A (p21, Cip1) /FL=gb:NM_00389.1 /gb:BC001275.1 /gb:BC001933.1 /gb:U03106.1 /gb:U226163.1 /gb:U09579.1 /gb:NM_025113.1 /FL=gb:NM_025113.1 /DEF=Homo sapiens hypothetical protein FLJ21562 (FLJ21562), mRNA. /FEA=mRNA /GEN=FLJ21562 /PROD=hypothetical protein FLJ21562
219471_at	gb:NM_025113.1 /FL=gb:NM_025113.1 /DEF=Homo sapiens hypothetical protein FLJ21562 (FLJ21562), mRNA. /FEA=mRNA /GEN=FLJ21562 /PROD=hypothetical protein FLJ21562
208651_x_at	gb:MSB6641 /DEF=Homo sapiens CD24 signal transducer mRNA, complete cds. /FEA=mRNA /PROD=signal transducer CD24 /DB_XREF=gi:180167 /UG-Hs_286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:MSB6641.9b:U33930.1 /gb:NM_01230.1
211431_s_at	gb:AF015524.1 /DEF=Homo sapiens putative chemokine receptor (CRAM-A) mRNA, complete cds. /FEA=mRNA /GEN=CRAM-A /PROD=putative chemokine receptor /DB_XREF=gi:3550066 /UG-Hs_302043 chemokine (C-C motif) receptor-like 2 /FL=gb:AF015524.1 /Consensus includes gb:AT857639 /FEA=mRNA /DB_XREF=est:wi95g09.x1 /CLONE=IMAGE:2423200 /UG-Hs_96
204285_s_at	phorbol-12-myristate-13-acetate-induced protein 1 /FL=gb:NM_021127.1 /Consensus includes gb:AA70170 /FEA=mRNA /DB_XREF=gi:1821408 /DB_XREF=est:ab84d09.s1 /CLONE=132321 /UG-Hs_288156 Homo sapiens cDNA: FLJ21819 f1s, Clone HEPO1185
219081_at	gb:NM_024668.1 /DEF=Homo sapiens hypothetical protein FLJ20288 (FLJ20288), mRNA. /FEA=mRNA /GEN=FLJ20288 /PROD=hypothetical protein FLJ11979 /DB_XREF=gi:13386461 /UG-Hs_84045 hypothetical protein FLJ20288 /FL=gb:BC004457.1 qb:NM_024668.1 /Consensus includes gb:NM_013399.1 /DEF=Homo sapiens VNN3 protein (HSA238982), mRNA. /FEA=mRNA /GEN=HSA238982 /PROD=VN33 protein /DB_XREF=gi:9055235 /UG-Hs_133656 VNN3 protein /FL=gb:NM_013399.1
220528_at	gb:NM_003519.1 /DEF=Homo sapiens carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. /FEA=mRNA /GEN=SLC22A4 /PROD=solutes carrier family 22 (organic cation transporter), member 4 /DB_XREF=gi:4507002 /UG-Hs_77239 solute carrier family 22 (organic cation transporter), member 4 /FL=gb:AB007448.1 qb:NM_003059.1
211445_x_at	gb:AF315951.1 /DEF=Homo sapiens FKSGL1 (FKSG17) mRNA, complete cds. /FEA=mRNA /GEN=FKSG17 /PROD=FKSG17 /DB_XREF=gi:12276119 /gb:NM_301057 Homo sapiens FKSGL1 (FKSG17) mRNA, complete cds /FL=gb:AF315951.1
204286_s_at	gb:NM_021127.1 /DEF=Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMIP1), mRNA. /FEA=mRNA /GEN=PMIP1 /PROD=phorbol-12-myristate-13-acetate-induced protein 1 /FL=gb:NM_021127.1
202503_s_at	gb:NM_014736.1 /DEF=Homo sapiens clone FLB8299 PRO2399 mRNA, complete cds. /FEA=mRNA /PROD=PRO2399 /DB_XREF=gi:11493529 /gb:NM_13013.1 /DEF=Homo sapiens clone FLB8299 PRO2399 mRNA, complete cds. /FEA=mRNA /GEN=KIAA0101 gene product /DB_XREF=gi:10863922 /UG-Hs_96 phorbol-12-myristate-13-acetate-induced protein 1 /FL=gb:NM_021127.1
211560_s_at	gb:BC000251.1 /DEF=Homo sapiens cytochrome b5 outer mitochondrial membrane precursor /FL=gb:AF31013.1 /UG-Hs_79103 cytochrome b5 outer mitochondrial membrane precursor /FL=gb:AF31013.1
209945_s_at	FEA=mRNA /PROD=Similar to glycogen synthase kinase 3 beta /DB_XREF=gi:12652980 /UG-Hs_78802 glycogen synthase kinase 3 beta /FL=gb:BC00251.1
217997_at	Consensus includes gb:AI795608 /FEA=mRNA /DB_XREF=gi:5361371 /DB_XREF=est:wh40a05.x1 /CLONE=IMAGE:2383184 /UG-Hs_82101 plectstrin homology-like domain, family A, member 1 /FL=gb:NM_007350.1
203757_s_at	gb:BC005058.1 /DEF=Homo sapiens, carinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), clone Mgc:10467, mRNA. /PROD=carinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) /DB_XREF=gi:13477106 /UG-Hs_73848 carinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) /FL=gb:BC005058.1 /gb:NM_002483.1
205269_at	Consensus includes gb:AI123251 /FEA=mRNA /DB_XREF=gi:35539017 /DB_XREF=est:ge47903.x1 /CLONE=INDGE:1689940 /UG-Hs_2488 lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76KD) /FL=gb:NM_005565.2 qb:NM_002483.1
219049_at	gb:NM_018371.1 /DEF=Homo sapiens hypothetical protein FLJ11264 (FLJ11264), mRNA. /FEA=mRNA /GEN=FLJ11264 /PROD=hypothetical protein FLJ11264
209396_s_at	gb:NM_0927.1 /DEF=Human glycoprotein mRNA, complete cds. /FEA=mRNA /PROD=glycoprotein /DB_XREF=gi:348911 /UG-Hs_75184 chitinase 3-like 1 (cartilage glycoprotein-39) /FL=gb:MB0927.1 qb:NM_001276.1
202637_s_at	Consensus includes gb:AI608725 /FEA=mRNA /DB_XREF=gi:46177892 /DB_XREF=est:tw90001.x1 /CLONE=IMAGE:2266921 /UG-Hs_168303 intercellular adhesion molecule 1 (CD54), human rhinovirus receptor /FL=gb:M24283.1 qb:J03132.1 qb:NM_000201.1
205557_at	gb:NM_001725.1 /DEF=Homo sapiens bacterial permeability-increasing protein (BPI), mRNA. /FEA=mRNA /GEN=BPI /PROD=bactericidal permeability-increasing protein precursor /DB_XREF=gi:4502446 /UG-Hs_89555 bactericidal permeability-increasing protein /FL=gb:AF322588.1 qb:J04739.1 qb:NM_001725.1
207072_at	gb:NM_003863.1 /DEF=Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), mRNA. /FEA=mRNA /GEN=IL18RAP /PROD=interleukin 18 receptor accessory protein /DB_XREF=gi:4504656 /UG-Hs_158315 interleukin 18 receptor accessory protein /FL=gb:AF077346.1 qb:NM_003853.1

202498_s_at	Consensus includes qb:BB550486 / DB_XREF=gi:9792178 / DB_XREF=est:j7a27c01.x1 / CLONE_IMAGE:3219936 /UG=Hs_784 solute carrier family 2 (facilitated glucose transporter), member 3 /FL=gb:M20581.1. qb:NM_006931.1
218739_at	qb:NM_016061.1 /DEF/Homo sapiens CG1-58 protein (LOC51099), mRNA. /GEN=LOC51099 /PRO=CG1-58 protein /DB_XREF=gi:7705770 /UG=Hs_19385 CG1-58 protein /FL=gb:AF151816.1. qb:NM_016061.1
212722_s_at	Consensus includes qb:AK021780.1 /DB/Homo sapiens cDNA FLJ1718 fis, clone HEMBA105232, highly similar to Homo sapiens mRNA for KIAA0385 protein. /FEA=mRNA /DB_XREF=gi:10433034 /UG=Hs_72660 phosphatidylserine receptor antigen identified by monoclonal antibodies /CLONE_IMAGE:3074568 /UG=Hs_20952 Homo sapiens clone 24411 mRNA sequence qb:NM_006111.1 /DEF/Homo sapiens CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EJ32 and G344) (CD59), mRNA. /FEA=mRNA /GEN=CD59 /PROD=CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EJ32 and G344) /FL=gb:NM_016631.64 /DB_XREF=gi:10433034 /UG=Hs_72660 phosphatidylserine receptor antigen identified by monoclonal antibodies /CLONE_IMAGE:3074568 /UG=Hs_20952 Homo sapiens clone 24411 mRNA sequence qb:NM_006111.1 /DEF/Homo sapiens tumor necrosis factor, alpha-induced protein 6 (TNEFIP6), mRNA. /FEA=mRNA /GEN=TNEFIP6 /PROD=tumor necrosis factor, alpha-induced protein 6 /FL=gb:NM_007115.1
210740_s_at	qb:AF279372.1 /DEF/Homo sapiens inositol 1,3,4-trisphosphate 5'-kinase mRNA, complete cds. /FEA=mRNA /PROD=inositol 1,3,4-trisphosphate 5'-kinase mRNA /DB_XREF=gi:12006345 /UG=Hs_6453 inositol 1,3,4-trisphosphate 56 kinase /FL=gb:AF279372.1
202333_s_at	Consensus includes qb:AA877765 /DB_XREF=gi:12986730 /DB_XREF=est:nr06f05.s1 /CLONE_IMAGE:1161057 /UG=Hs_811 ubiquitin-conjugating enzyme E2B (RAD6 homolog) /FL=gb:M7455.1. qb:NM_00333.1
201566_x_at	qb:DI3899.1 /DEF/Human mRNA for Id-2H, complete cds /FEA=mRNA /GEN=Id-2H /DB_XREF=gi:464183 /UG=Hs_180919 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /FL=gb:NM97796.1. qb:NM_002166.1 /db:G3891.1 Cluster Inc. AI129310.1:g48ao5.x1 Homo sapiens cDNA, 3 end /Clone=IMAGE-11212816 /clone_end=3 /gb=AI129310 /gi=3597824 /ug=Hs_234923 /len=811
213836_s_at	Consensus includes qb:AN052084 /FEA=EST /DB_XREF=gi:15914443 /DB_XREF=est:ny86707.x1 /CLONE_IMAGE:2555461 /UG=Hs_279937 KIBA1001 protein
205027_s_at	qb:NM_005204.1 /DEF/Homo sapiens mitogen-activated protein kinase kinase kinase 8 (MAP3K8), mRNA. /FEA=mRNA /GEN=MAP3K8 /PROD=mitogen-activated protein kinase kinase kinase /DB_XREF=gi:4885146 /UG=Hs_248 mitogen-activated protein kinase kinase kinase 8 /FL=gb:D14497.1 qb:NM_005204.1
207329_at	qb:NM_002424.1 /DEF/Homo sapiens matrix metalloproteinase 8 (neutrophil collagenase) (MMP8), mRNA. /FEA=mRNA /GEN=MMP8 /PROD=matrix metalloproteinase 8 preproprotein /FL=gb:J05556.1 qb:NM_002424.1
217996_at	Consensus includes qb:AA576361 /FEA=EST /DB_XREF=gi:235435 /DB_XREF=est:im82408.s1 /CLONE_IMAGE:1074735 /UG=Hs_82101 pleckstrin homology-like domain, family A, member 1 /FL=gb:NM_007350.1
208632_at	Consensus includes qb:AL578551 /FEA=EST /DB_XREF=gi:12942733 /DB_XREF=est:AL578551 /CLONE=CSOK001YG01 (3 prime) /qb:NM_5094 ring finger protein 10 /FL=gb:AB027195.1
206851_at	qb:NM_002935.1 /DEF/Homo sapiens ribonuclease, RNase A family, 3 (eosinophil cationic protein) (RNASE3), mRNA. /FEA=mRNA /GEN=RNASE3 /PROD=ribonuclease, RNase A family, 3 (eosinophil cationic protein) /DB_XREF=gi:4506550 /UG=Hs_72839 ribonuclease, RNase A family, 3 (eosinophil cationic protein) /FL=gb:NM_002935.1 qb:M281128.1
203434_s_at	Consensus includes qb:AA143363 /DB_XREF=gi:4289355 /DB_XREF=est:l165g1.x1 /CLONE_IMAGE:2136932 /UG=Hs_1298 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, cathepsin D), mRNA. /FL=gb:NM_007287.1 qb:NM_007288.1
216236_s_at	Consensus includes qb:AU110298.1 /DEF=Homo sapiens mRNA; CDNA DKF56AK1672 (from clone DKF56AK1672); partial cds. /FEA=mRNA /GEN=DKF56AK1672 /PROD=hypothetical protein /DB_XREF=gi:5817238 /UG=Hs_7504 solute carrier family 2 (facilitated glucose transporter), member 3
206342_x_at	qb:NM_006123.1 /DEF/Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 2, mRNA. /FEA=mRNA /GEN=IDS /PROD=iduronate-2-sulfatase isofrom b precursor /DB_XREF=gi:5366207 /UG=Hs_172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:LA0586.1 qb:NM_006123.1
201329_s_at	qb:NM_005239.1 /DEF/Homo sapiens v-ets avian erythroblastosis virus E26 oncogene homolog 2 (ETS2), mRNA. /FEA=mRNA /GEN=ETS2 /PROD=v-ets avian erythroblastosis virus E26 oncogene homolog 2 /DB_XREF=gi:4885220 /UG=Hs_85146 v-ets avian erythroblastosis virus E26 oncogene homolog 2 /FL=gb:J04102.1 qb:NM_005239.1
200731_s_at	Consensus includes qb:AW165960 /FEA=EST /DB_XREF=gi:6397485 /DB_XREF=est:xk43a12.x1 /CLONE_IMAGE:2620798 /UG=Hs_227777 protein tyrosine phosphatase type IVA, member 1 /FL=gb:U4689.1 qb:NM_003163.1
212508_at	Consensus includes qb:AK021029.1 /DEF=Homo sapiens cDNA FLJ13967 fis, clone Y79AA1001402, weakly similar to Homo sapiens paraneoplastic cancer-testis-brain antigen (MA1) mRNA. /FEA=mRNA /DB_XREF=gi:10436287 /UG=Hs_24719 modulator of apoptosis 1 /

37028_at	Cluster Incl. U83981:Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds /cds=[/222,2246] /gb=U83981 /gi=32258617 /ug=Hs.76556 /len=231
40446_at	Cluster Incl. AU021366:cICR0721Q.4.1 (PHD finger protein 2) (isoform 2) /cds=[/215,1918] /gb=AU021366 /gi=3169115 /ug=Hs.166204 /len=2260
21902_s_at	gb:NM_017742.1 /DEF=Homo sapiens hypothetical protein FLJ20281 /DB XREF=gi:8923259 /UG=Hs.18800 mRNA. /FEA=mRNA /GEN=FLJ20281 /PROD=hypothetical protein FLJ20281 /mRNA. /FEA=mRNA /GEN=FLJ20281
202158_s_at	gb:NM_006561.1 /DEF=Homo sapiens CUG triplet repeat, RNA-binding protein 2 (CUGBP2), mRNA. /FEA=mRNA /GEN=CUGBP2 /PROD=CUG triplet repeat, RNA-binding protein 2 /DB_XREF=gi:5729815 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FI=gb:U95546.1 gb:AF036956.1_gb:AF09064.1_gb:NM_006561.1
60081_at	Cluster Incl. AI453099:t16ie11_x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2146028 /clone_end=3 /gb=A1453099 /gi=4307988.24668 /len=554
210142_x_at	gb:AF117234.1 /DEF=Homo sapiens flotillin mRNA, complete cds. /FEA=mRNA /PROD=flotillin /DB_XREF=gi:6563241 /UG=Hs.179966 Flotillin 1 /FI=gb:AF117234.1
204490_s_at	gb:M24915.1 /DEF=Human Cd44 antigen, complete cds. /FEA=mRNA /DB_XREF=gi:180196 /UG=Hs.169610 CD44 antigen (homing function and Indian blood group system) /FI=gb:NN.00610.1_gb:NN.U4073.1_gb:NM2040.1_gb:MB21915.1
203949_at	gb:NM_0002305.1 /DEF=Homo sapiens myeloperoxidase (MPO), nuclear gene encoding mitochondrial protein mRNA. /FEA=mRNA /GEN=MPO /PROD=myeloperoxidase /DB_XREF=gi:4557758 /UG=Hs.1817 myeloperoxidase /FL-gb:m19507.1 /gb:J02694.1_gb:NN.000250.1
219239_at	gb:NM_022367.1 /DEF=Homo sapiens hypothetical protein FLJ12287 similar to semaphorins (FLJ12287), mRNA. /FEA=mRNA /GEN=FLJ12287 /PROD=hypothetical protein FLJ12287 similar to semaphorins /FL-gb:NN.022367.1_gb:XREF=gi:11641290 /UG=Hs.7634 hypothetical protein FLJ12287 similar to semaphorins /FI=gb:NN.022367.1_gb:ABU2939.1
201751_at	gb:NM_014876.1 /DEF=Homo sapiens KIAA0063 gene product (KIAA0063) mRNA. /FEA=mRNA /GEN=KIAA0063 /PROD=KIAA0063 gene product /DB_XREF=gi:7661887 /UG=Hs.3034 KIAA0063 gene product /EU=gb:D31084.1_gb:NM_014876.1
203153_at	gb:NM_001548.1 /DEF=Homo sapiens interferon-induced protein with tetra-tricopeptide repeats 1 (IFT11) mRNA.. /FEA=mRNA /GEN=IFT11 /PROD=interferon-induced protein with tetra-tricopeptide repeats 1 /DB_XREF=gi:4544584 /UG=Hs.20315 interferon-induced protein with tetra-tricopeptide repeats 1 /FI=gb:NM_001548.1
210724_at	gb:AF239761.1 /DEF=Homo sapiens EG-like module-containing mucin-like receptor EMR3 mRNA, complete cds. /FEA=mRNA /PROD=EG-like module-containing mucin-like receptor EMR3 mRNA, complete cds /FI=gb:AF239764.1 /UG=Hs.326777 Homo sapiens EG-like module-containing mucin-like receptor EMR3 mRNA, complete cds /EU=gb:AF239764.1
202381_at	gb:NM_003816.1 /DEF=Homo sapiens a disintegrin and metalloprotease domain 9 (meltrin gamma) (ADAM9), mRNA. /FEA=mRNA /GEN=ADAM9 /PROD=a disintegrin and metalloprotease domain 9 (meltrin gamma) /EU=gb:gi:14501914 /UG=Hs.2442 a disintegrin and metalloprotease domain 9 (meltrin gamma) /FI=gb:NN.003816.1_gb:NM_003816.1
217624_at	Consensus includes gb:NM_0050009 /FEA=EST /DB_XREF=gi:7112213 /DB_XREF=est:UT-HF-BN0-ali-e-0-0-U..rl /CLONE=IMAGE-3077105 /UG=Hs.184325 CGI-76 protein /EU=gb:AF151834.1_gb:AF151039.1_gb:NM_016021.1
200984_s_at	Consensus includes gb:X1647.1 /DEF=Human protein for DB9, an Ig-6-like protein regulating membrane attack. /FEA=mRNA /PROD=precursor polypeptide (AA -25 to 103) /DB_XREF=gi:29805 /UG=Hs.1116663 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.345, EJ16, EJ30, EL32 and G34) /FI=gb:NN.000611.1_gb:NM_016021.1
219999_at	gb:NM_018621.1 /DEF=Homo sapiens hypothetical protein PRO2198 (PRO2198), mRNA. /FEA=mRNA /GEN=PRO2198 /PROD=hypothetical protein PRO2198 /DB_XREF=gi:8924129 /UG=Hs.116459 hypothetical protein PRO2198 /FI=gb:AF116691.1_gb:NM_018621.1
212644_s_at	Consensus includes gb:AI67174 /FEA=EST /DB_XREF=gi:4851478 /DB_XREF=est:w005e6.x1 /CLONE=IMAGE-2297218 /UG=Hs.81360 Homo sapiens cDNA: FLJ21927 fis, clone HEPO178, highly similar to HSU90909 Human clone 23172 mRNA sequence
219622_at	gb:NM_017817.1 /DEF=Homo sapiens hypothetical protein FLJ20429 (FLJ20429), mRNA. /FEA=mRNA /GEN=FLJ20429 /PROD=hypothetical protein FLJ20429 /DB_XREF=gi:8923400 /UG=Hs.179791 hypothetical protein FLJ20429 /EU=gb:NM_017817.1
219190_s_at	gb:NM_017629.1 /DEF=Homo sapiens hypothetical protein FLJ20033 (FLJ20033), mRNA. /FEA=mRNA /GEN=FLJ20033 /PROD=hypothetical protein FLJ20033 /FI=gb:NN.017629.1
208707_at	Consensus includes gb:BE552334 /FEA=EST /DB_XREF=gi:8923033 /UG=Hs.134757 hypothetical protein FLJ20033 /FI=gb:NN.017629.2
218506_x_at	/UG=Hs.286236 eukaryotic translation initiation factor 5 /FI=gb:NN.018459.1 /DEF=uncharacterized bone marrow protein BM045 /DB_XREF=gi:8922103 /GEN=BM045 /PROD=uncharacterized bone marrow protein BM045 /mRNA. /FEA=mRNA /GEN=BM045 /PROD=uncharacterized bone marrow protein BM045 /DB_XREF=gi:9194026 /DB_XREF=gi:8920102.1
207545_s_at	/UG=Hs.8750 uncharacterized bone marrow protein BM045 /EU=gb:AF17521.1_gb:NM_018459.1 /FEA=mRNA /GEN=NUMB /PROD=numb (Drosophila) homolog (NUMB), mRNA. /FEA=mRNA /GEN=NUMB /PROD=numb (Drosophila) homolog /FI=gb:NN.003744.1_gb:L40393.1_DB_XREF=gi:4505478 /UG=Hs.78830 numb (Drosophila) homolog /FI=gb:NN.003744.1_gb:L40393.1

212014_x_at	Consensus includes gb:AY493245 / FEA=EST / DB_XREF=gi:14394248 / DB_XREF=est:t130d08.x1 / CLONE=IMAGE:2131983 /UG-Hs.169610 CD44 antigen (homing function and Indian blood group system)
209039_x_at	gb:AF001434.1 /DEF=Human IgEast (IgEAST) mRNA, complete cds. /FEA=mRNA /GEN=IgEAST /PROD=Igast /DB_XREF=gi:2529706 /UG-Hs.155119 EH domain containing 1 /FL=gb:AF001434.1
208650_s_at	Consensus includes gb:BG327863 / FEA=EST / DB_XREF=gi:13134301 /DB_XREF=est:602426876f1 / CLONE=IMAGE:4564675 /UG-Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:MS8664.1 qb:NW_013230.1 qb:BC00893.1 /DEF=Homo sapiens H2B histone family member A /DB_XREF=gi:12654150 /UG-Hs.247817 H2B histone family, member A /ET=gb:BC00893.1 /PROD=H2B histone family member A /DB_XREF=gi:12654150 /UG-Hs.247817 H2B histone family, member A /ET=gb:BC00893.1
209806_at	Consensus includes gb:AF13147.1 / DEF=Homo sapiens clone 24951 mRNA sequence. / FEA=mRNA /DB_XREF=gi:4406562 /UG-Hs.167115 KIAA0330 protein
212573_at	Consensus includes gb:AV727449 / FEA=EST / DB_XREF=est:AV727449 / CLONE=HTCAYG01 /UG-Hs.199061 p300CBP-associated factor /ET=gb:U57317.2 qb:NW_003884.2
203845_at	Consensus includes gb:MI3231.1 / DEF=Human T-cell receptor aberrantly rearranged gamma-chain mRNA from cell line HEp-MIT. /FEA=mRNA /DB_XREF=gi:339168 /UG-Hs.274509 T cell receptor gamma constant 2 /DB_XREF=gi:016040.1 HOMO sapiens CGI-100 protein (LOC50999), mRNA. /FEA=mRNA /GEN=LOC50999 /PROD=CGI-100 protein /DB_XREF=gi:7705583 /UG-Hs.296155 CGI-100 protein /FL=gb:AF151658.1 qb:NW_016040.1 qb:NW_002094.1 /DEF=Homo sapiens G1 to S phase transition 1 (GSTP1), mRNA. /FEA=mRNA /GEN=GSTP1 /PROD=G1 to S phase transition 1 /DB_XREF=gi:4504166 /UG-Hs.2707 G1 to S phase transition 1 /FL=gb:NW_002094.1 qb:NW_006267.2 /DEF=Homo sapiens RAN binding protein 2 (RANBP2), mRNA. /FEA=mRNA /GEN=RANBP2 /PROD=RAN binding protein 2 /DB_XREF=gi:3382078 /UG-Hs.199179 RAN binding protein 2 /FL=gb:NW_006267.2 qb:D42063.1
202195_s_at	Consensus includes gb:NM_016540.1 HOMO sapiens CGI-100 protein (LOC50999), mRNA. /FEA=mRNA /GEN=LOC50999 /PROD=CGI-100 protein /DB_XREF=gi:7705583 /UG-Hs.296155 CGI-100 protein /FL=gb:AF151658.1 qb:NW_016040.1 qb:NW_002094.1 /DEF=Homo sapiens G1 to S phase transition 1 (GSTP1), mRNA. /FEA=mRNA /GEN=GSTP1 /PROD=G1 to S phase transition 1 /DB_XREF=gi:4504166 /UG-Hs.2707 G1 to S phase transition 1 /FL=gb:NW_002094.1 qb:NM_005502.1 /DEF=Homo sapiens Arp-binding cassette, sub-family A (ABC1), member 1 (ABC1), mRNA. /FEA=mRNA /GEN=ABC1 /PROB=Arp-binding cassette, sub-family A member 1 /DB_XREF=gi:5915657 /UG-Hs.2111562 ATP-binding cassette, sub-family A (ABC1), member 1 /FL=gb:AF165281.1 qb:NW_005502.1 qb:AF255167.1 /PROD=CDS2 protein /DB_XREF=gi:4186022 /UG-Hs.24812 CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 qb:NM_005502.1 /DEF=Homo sapiens Arp-binding cassette, sub-family A member 1 (ABC1), member 1 (ABC1), mRNA. /FEA=mRNA /GEN=ABC1 /PROB=Arp-binding cassette, sub-family A (ABC1), member 1 /DB_XREF=gi:5915657 /UG-Hs.2111562 ATP-binding cassette, sub-family A (ABC1), member 1 /FL=gb:AF165281.1 qb:NW_005502.1 qb:AF255167.1
203504_s_at	Consensus includes gb:Y16521.1 /DEF=Homo sapiens mRNA for CDS2 protein. /FEA=mRNA /GEN=cds2 /PROD=CDS2 protein /DB_XREF=gi:4186022 /UG-Hs.24812 CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 qb:NM_005502.1 /DEF=Homo sapiens Arp-binding cassette, sub-family A (ABC1), member 1 (ABC1), mRNA. /FEA=mRNA /GEN=ABC1 /PROB=Arp-binding cassette, sub-family A (ABC1), member 1 /DB_XREF=gi:5915657 /UG-Hs.2111562 ATP-binding cassette, sub-family A (ABC1), member 1 /FL=gb:AF165281.1 qb:NW_005502.1 qb:AF255167.1
212457_at	Consensus includes gb:AI161985.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761J1810 (from clone DKFZp761J1810). /FEA=mRNA qb:NW_002812.1 /UG-Hs.274184 transcription factor binding to IGH enhancer 3
214683_s_at	Consensus includes gb:AI251890 / FEA=EST /DB_XREF=est:qu78d12.x1 /CLONE=IMAGE:1978199 /UG-Hs.2083 CDC-like kinase1
14783_s_at	Cluster Inc1. R61377:y115e02.51 Homo sapiens cDNA, 3 end /clone=IMAGE-37665 /clone_end=3 /gb:R613774 /gi:832069 /ug=1 /id=24434 /len=34
202232_at	gb:NW_002870.1 /DEF=Homo sapiens RAS oncogene family /DB_XREF=gi:4506362 /UG-Hs.151536 RAB13, member RAS oncogene family /FL=gb:BC000799.1 qb:NW_002870.1
206025_s_at	Consensus includes gb:AW188198 / FEA=EST /DB_XREF=gi:64262634 /DB_XREF=est:t1931503.x1 /CLONE=IMAGE:2664197 /UG-Hs.29352 tumor necrosis factor, alpha-induced protein 6 /FL=gb:NW_001115.1
203936_s_at	gb:NW_004994.1 /DEF=Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) (MMP9), mRNA. /FEA=mRNA /GEN=MMP9 /PROD=matrix metalloproteinase 9 preproprotein /DB_XREF=gi:4826835 /UG-Hs.151738 matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase).
221523_s_at	Consensus includes gb:AI138717 /DEF=Human DNA conjugating enzyme UBC6 homolog, the gene for a possible GTP binding protein, NACA (nascent-polypeptide-associated complex alpha polype... /UG-Hs.2386719 Rag D protein /FL=gb:NW_021244.1 qb:AF272036.1 qb:BC003088.1
215705_s_at	Consensus includes gb:AI161991.1 /DEF=Homo sapiens /FEA=mRNA /GEN=DEFZp61H087 /PROD=hypothetical protein /DB_XREF=gi:7328000 /UG-Hs.258503 p53 inducible protein partial cds. /FEA=mRNA /GEN=DEFZp61H087 /PROD=hypothetical protein NpBP (LOC51729), mRNA. /FEA=mRNA /GEN=LOC51729 /PROD=NpBP-binding protein NpBP /DB_XREF=gi:706500 /UG-Hs.16420 NpBP-binding protein NpBP /FL=gb:BC001621.1 qb:AF118023.1 qb:AB029309.1 qb:NW_016312.1
202206_at	Consensus includes gb:AW450363 / FEA=EST /DB_XREF=gi:6991139 /DB_XREF=est:U1-H-BI3-akn-d-02-0-UT.s1 /CLONE=IMAGE:2734875 /UG-Hs.111554 ADP-ribosylation factor-like 7 /FL=gb:BC001051.1 qb:AB01681.1 qb:NW_005737.2 qb:NW_000202.2 /DEF=Homo sapiens Iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA. /FEA=mRNA /GEN=IDS /PROD=iduronate 2-sulfatase isoform a precursor /DB_XREF=gi:53600215 /UG-Hs.172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:NM_000202.2

213056_at	Consensus includes gb:AU145019 / DB_XREF=gi:11006540 / DB_XREF=est:AU145019 / CLONE=IMAGE:MEMBR1003646 /UG-Hs_96427 KIAA1013 protein
222142_at	Consensus includes gb:AK024212.1 / DEF=Homo sapiens cDNA FLJ14150 firs, clone MAMMAL03026, highly similar to Homo sapiens HSP0257 mRNA. /FEA=mRNA /DB_XREF=gi:10436534 /UG-Hs_18827 KIAA0849 protein
214784_x_at	Consensus includes gb:BE966299 / DB_XREF=gi:11771566 /DB_XREF=est:601660539R1 /CLONE=IMAGE:3906248 /UG-Hs_70500 KIAA0310 protein
222035_s_at	Consensus includes gb:AL984479 / DB_XREF=gi:5811756 /DB_XREF=est:wT83e06.x1 /CLONE=IMAGE:2194306 [UG=Hs_49007 Poly(A) Polymerase alpha]
212219_at	Consensus includes gb:D38521.1 / DEF=Human mRNA for KIAA0077 gene, partial cds. /FEA=mRNA /GEN=KIAA0077 /DB_XREF=gi:559329 /UG-Hs_112396 KIAA0077 protein
214152_at	Consensus includes gb:AU144243 / DB_XREF=est:AU144243 /CLONE=HEMBAL001328 /UG-Hs_247118 phosphatidylinositol glycan, class B
202948_at	gb:NM_000877.1 / DEF=Homo sapiens interleukin 1 receptor, type I (IL1RI), mRNA. /FEA=mRNA /GEN=IL1RI /PROD=interleukin 1 receptor, type I /DB_XREF=gi:4504658 /UG-Hs_82112 interleukin 1 receptor, type I (IL1RI), mRNA. /FEA=mRNA /GEN=NR4A3 /PROD=nuclear receptor subfamily 4, group A, member 3 /DB_XREF=gi:11276070 /UG-Hs_80561 nuclear receptor subfamily 4, group A, member 3 /FL=gb:NM_006381.1 gb:D78579.1
207978_s_at	gb:NM_00981.1 / DEF=Homo sapiens nuclear receptor subfamily 4, group A, member 3 /DB_XREF=gi:11276070 /UG-Hs_80561 nuclear receptor subfamily 4, group A, member 3 /FL=gb:NM_006381.1 gb:D78579.1
209304_x_at	gb:AF081853.1 / DEF=Homo sapiens growth arrest and DNA damage inducible protein beta (GADD45B) mRNA, complete cds. /FEA=mRNA /GEN=GADD45B /PROD=growth arrest and DNA damage inducible, beta /FL=gb:AF081853.1 gb:AF081807.1
214783_s_at	Consensus includes gb:BG177920 / DB_XREF=est:602327839F1 /CLONE=IMAGE:4429256 /UG-Hs_75510 annexin A11
46270_at	Cluster ID: AL039447 /DEF=Zfp434N1010_s1 Homo sapiens cDNA, 3 end /clone=DKFzp434N1010 /clone_end=3 /gb=AL039447 /gi:5408497 /ug=Hs_75425 /en=841
221760_at	Consensus includes gb:BG287153 /DB_XREF=est:602381868F1 /CLONE=IMAGE:4499393 /UG-Hs_25253 mannose-dase, alpha, class 1A, member 1
210118_s_at	gb:NM_015329.1 / DEF=Human interleukin 1 (IL1A) mRNA, complete cds. /FEA=mRNA /GEN=IL1A /PROD=interleukin 1-alpha /DB_XREF=gi:186277 /UG-Hs_1722 interleukin 1, alpha /FL=gb:NM_015329.1
204781_s_at	gb:NM_00043.1 / DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), mRNA. /FEA=mRNA /GEN=TNFRSF6 /PROD=apoptosis (APO-1) antigen 1 /DB_XREF=gi:4507582 /UG-Hs_82359 tumor necrosis factor receptor superfamily, member 6 /FL=gb:NM_00043.1
207677_s_at	gb:NM_013416.1 / DEF=Homo sapiens neutrophil cytosolic factor 4 (NCF4), transcript variant 2, mRNA. /FEA=mRNA /GEN=NCF4 /PROD=neutrophil cytosolic factor 4 (NCF4), transcript variant 4 (40KD) (NCF4), isoform 2 /DB_XREF=gi:382492 /UG-Hs_196352 neutrophil cytosolic factor 4 (40KD) /FL=gb:BC002798.1 gb:AB025219.1 qb:NM_013416.1
206302_s_at	gb:NM_019091.1 / DEF=Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDIX), mRNA. /FEA=mRNA /GEN=NUDIX /PROD=nudix (nucleoside diphosphate linked moiety X)-type motif 4 /DB_XREF=gi:108600138 /UG-Hs_92381 nudix (nucleoside diphosphate linked moiety X)-type motif 4 /FL=gb:NM_019094.1 qb:AF191619.1 qb:AF191650.1 qb:AE191653.1
219450_s_at	gb:NM_017849.1 / DEF=Homo sapiens hypothetical protein FLJ2050507 (FLJ2050507) mRNA. /FEA=mRNA /GEN=FLJ2050507 /PROD=hypothetical protein FLJ2050507
212225_at	Consensus includes gb:AL518854 /DB_XREF=est:AL516854 /CLONE=CSOBA007YB20 (5 prime) /UG-Hs_150560 putative translation initiation factor
204479_at	gb:NM_012383.1 / DEF=Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /FEA=mRNA /GEN=OSTF1 /PROD=osteoclast stimulating factor 1 /DB_XREF=gi:692563 /UG-Hs_95821 osteoclast stimulating factor 1 /FL=gb:163717.1 qb:NM_012383.1
216457_s_at	Consensus includes gb:NM_012383.1 / DEF=Homo sapiens cDNA: FLJ22427 firs, clone HRC0913. /FEA=mRNA /DB_XREF=gi:10438814 /UG-Hs_288883 splicing factor 3a, subunit 1, 120KD
212266_at	Consensus includes gb:AM293356 /DB_XREF=est:DB_XREF=gi:66999992 /DB_XREF=est:U1-H-B12-ah1-c-11-0-U1-S1 /CLONE=IMAGE:272765 /UG-Hs_58220 Homo sapiens cDNA: FLJ23005 firs, clone LNG00396, highly similar to AF050223 Homo sapiens clone 24723 mRNA sequence
203675_at	gb:NM_005013.1 / DEF=Homo sapiens nucleobindin 2 (NUCB2), mRNA. /FEA=mRNA /GEN=NUCB2 /PROD=nucleobindin 2 /DB_XREF=gi:4826869 /UG-Hs_3164 nucleobindin 2 /FL=gb:AF052642.1 qb:AF052643.1 qb:AF052644.1 qb:NM_005013.1
221156_x_at	gb:NM_004748.1 / DEF=Homo sapiens cell cycle progression 8 protein (CPBP), mRNA. /FEA=mRNA /GEN=CPBP /PROD=cell cycle progression 8 protein /DB_XREF=gi:4758047 /UG-Hs_283153 cell cycle progression 8 protein /FL=gb:AF011794.1 qb:NM_001748.1
207791_s_at	gb:NM_004161.1 / DEF=Homo sapiens RAB1, member RAS oncogene family (RAB1), mRNA. /FEA=mRNA /GEN=RAB1 /PROD=RAB1,

	member RAS oncogene family /DB_XREF=gi:4758987 /UG=Hs.3642 RAB1, member RAS oncogene family /EL=gb:NM_004161.1 gb:M8209.1	
200692_s_at	gb:NM_004134.1 /DEF=Homo sapiens heat shock 70kD protein 9B (mortalin-2) /HSRPRB, mRNA. /FEA=mRNA /GEN=JSP9B /PROD=heat shock 70kD protein 9B (mortalin-2) /DB_XREF=gi:4758569 /UG=Hs.3069 heat shock 70kD protein 9B (mortalin-2) /EL=gb:IC000478.1 gb:L15189.1 gb:NM_004134.1	
218936_s_at	gb:NM_014167.1 /DEF=Homo sapiens HSPC128 protein (HSPC128) /mRNA. /FEA=mRNA /GEN=HSPC128 /PROD=HSPC128 protein /DB_XREF=gi:7661789 /UG=Hs.90527 HSPC128 protein /EL=gb:AF213377.1 gb:NM_014167.1	
213931_at	Consensus includes gb:AB19238 /FEA=EST /DB_XREF=gi:1:5438328 /DB_XREF=est:w42505.x1 /CLONE=IMAGE:24055528 /UG=Hs.180919 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein gb:NM_016626.1 /DEF=Homo sapiens hypothetical protein /LOC51320, mRNA. /FEA=mRNA /GEN=LOC51320 /PROD=hypothetical protein /DB_XREF=gi:1706165 /UG=Hs.18280 hypothetical protein /EL=gb:AF208855.1 gb:NM_016626.1	
218247_s_at	Consensus includes gb:AF07132.1 /DEF=Homo sapiens clone 23551 mRNA sequence. /FEA=mRNA /DB_XREF=gi:2852606 /UG=Hs.184019 Homo sapiens clone 23551 mRNA sequence. gb:AB023420.1 /DEF=Homo sapiens mRNA for heat shock protein apg-2, complete cds. /FEA=mRNA /GEN=apg-2 /PROD=apg-2 /DB_XREF=gi:4579908 /UG=Hs.90093 heat shock 70kD protein 4 /EL=gb:AB023420.1	
218177_at	Consensus includes gb:AB293502 /FEA=EST /DB_XREF=gi:1941036 /DB_XREF=est:zt53n06.r1 /CLONE=IMAGE:726107 /UG=Hs.42733 CHMP1.5 protein /EL=gb:AF281064.1 gb:NM_020112.1	
200648_s_at	gb:NM_002065.1 /DEF=Homo sapiens glutamate-ammonia ligase (glutamine synthetase) (GUN1), mRNA. /FEA=mRNA /GEN=GUN1 / PROD=glutamate-ammonia ligase (glutamine synthetase) /FL=gb:NM_002065.1 glutamate-ammonia ligase (glutamine synthetase) /FL=gb:NM_002065.1	
202843_at	gb:NM_012328.1 /DEF=Homo sapiens microvascular endothelial differentiation gene 1 (MDGI), mRNA. /FEA=mRNA /GEN=MDGI / PROD=microvascular endothelial differentiation gene 1 (MDGI), mRNA. /UG=Hs.6790 DnaJ (Hsp40) homolog, subfamily B, member 9 /EL=gb:AE003247.1 gb:AB026908.1 gb:NM_012328.1	
214578_s_at	Consensus includes gb:AV683882 /FEA=EST /DB_XREF=gi:10285745 /DB_XREF=est:AV683882 /CLONE=GKCATC05 /UG=Hs.17820 Rho-associated, coiled-coil containing protein kinase 1 /EL=gb:U3195.1 gb:NM_005406.1	
217473_x_at	Consensus includes gb:AF229163 /DEF=Homo sapiens natural resistance-associated macrophage protein 1 (SIC111) gene, complete cds, alternatively spliced; and nuclear LIM interactor-interacting factor (NLI-IF) gene, complete cds / FEA=mRNA_3 /DB_XREF=gi:102574038 /UG=Hs.182611 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	
207624_s_at	gb:NM_000328.1 /DEF=Homo sapiens retinoblastoma GTPase regulator (RB1), mRNA. /FEA=mRNA /GEN=RB1 /PROD=retinoblastoma GTPase regulator / EL=gb:U5762.1 gb:NM_000328.1	
202778_s_at	gb:NM_003453.1 /DEF=Homo sapiens zinc finger protein 198 (ZNF198), mRNA. /FEA=mRNA /GEN=ZNF198 /PROD=zinc finger protein 198 /DB_XREF=gi:4506010 /UG=Hs.10926 zinc finger protein 198 /EL=gb:AE035374.1 gb:NM_003453.1	
200653_s_at	gb:NM_018310.1 /DEF=Human calmodulin mRNA, complete cds /FEA=mRNA /PROD=calmodulin /DB_XREF=gi:179809 /UG=Hs.117656 calmodulin 1 (phosphorylase kinase, delta) /EL=gb:M27319.1 gb:NM_018310.1 gb:NM_006888.1	
218677_at	gb:NM_018310.1 /DEF=Homo sapiens hypothetical protein FLJ11259 (FLJ11259), mRNA. /FEA=mRNA /GEN=FLJ11259 /PROD=hypothetical protein FLJ11259 /DB_XREF=gi:822957 /UG=Hs.18465 hypothetical protein FLJ11259 (FLJ11259), mRNA. /FEA=mRNA /GEN=FLJ11259 /PROD= 202059_s_at	gb:NM_002264.1 /DEF=Homo sapiens karyopherin alpha 1 (importin alpha 5) (KPN1), mRNA. /FEA=mRNA /GEN=KPN1 /PROD= karyopherin alpha 1 /DB_XREF=gi:4504894 /UG=Hs.1694.9 karyopherin alpha 1 (importin alpha 5) /FL=gb:BC002374.1 gb:BC003009.1 gb:NM_002264.1
218132_s_at	gb:NM_024075.1 /DEF=Homo sapiens LENG5 protein (LENG5), mRNA. /FEA=mRNA /GEN=LENG5 /PROD=LENG5 protein / DB_XREF=gi:13129061 /UG=Hs.15560 LENG5 protein /EL=gb:BC000944.2 gb:NM_024075.1	
203265_s_at	Consensus includes gb:AB810268 /FEA=EST /DB_XREF=gi:2879627 /DB_XREF=est:cd1af07.s1 /CLONE=IMAGE:1367941 / UG=Hs.75217 mitogen-activated protein kinase kinase 4 /EL=gb:NM_003010.1 gb:U17713.1	
209634_at	gb:N97655.1 /DEF=Human 6-pyruvoyltetrahydropterin synthase (PTS) mRNA, complete cds. /FEA=mRNA /GEN=PTS / PROD=6-pyruvoyltetrahydropterin synthase (PTS) mRNA, complete cds. /FEA=mRNA /GEN=PTS / EL=gb:N97655.1 gb:NM_000317.1 gb:U17400.1	
217391_at	Consensus includes gb:BF752121 /FEA=EST /DB_XREF=gi:120401032 /DB_XREF=est:bx12e01.x1 /CLONE=bx12e01 / UG=Hs.272108 ESTs	
222309_at	Consensus includes gb:MW972292 /FEA=EST /DB_XREF=gi:8162138 /DB_XREF=est:EST384381 /UG=Hs.292998 ESTs	

201027_s_at	gb:NM_005542.1 /DEF=Homo sapiens insulin induced gene 1 (INSIG1), mRNA. /FEA=mRNA /GEN=INSIG1 /PROD=Insulin induced gene 1 /DB_XREF=gi:5031800 /UG=Hs.56205 insulin induced gene 1 /EL=gb:NM_005542.1
211749_x_at	Consensus includes gb:AC004544 /DEF=Homo sapiens BAC clone CTB-162B4 from 4 /FEA=CD5 /DB_XREF=gi:3041843 /UG=Hs.248095 Homo sapiens BAC clone CTB-162B4 from 4
220496_at	gb:NM_016509.1 /DEF=Homo sapiens C-type lectin-like receptor-2 /LOC512661, mRNA. /FEA=mRNA /GEN=LOC51266 /PROD=C-type lectin-like receptor-2 /DB_XREF=gi:7706060 /UG=Hs.114231 C-type lectin-like receptor-2 /EL=gb:AF124841.1
201096_s_at	Consensus includes gb:AL537042 /FEA=EST /DB_XREF=gi:128000535 /DB_XREF=est:AL537042 /CLONE=CS0DF017/FL17 (5 prime) /UG=Hs.75290 ADP-ribosylation factor 4 /EL=gb:BC003361.1 gb:M36341.1 gb:NM_001660.2
201580_s_at	Consensus includes gb:AL544094 /FEA=EST /DB_XREF=gi:12875753 /DB_XREF=est:AL544094 /CLONE=CS0DT004/YG20 (3 prime) /UG=Hs.169358 hypothetical protein /EL=gb:NM_021156.1
201109_s_at	Consensus includes gb:AV726673 /FEA=EST /DB_XREF=gi:10836094 /DB_XREF=est:AV726673 /CLONE=HTCBGC12 /UG=Hs.87409 thrombospondin 1 /FL=gb:NM_003246.1
203080_s_at	gb:NM_0133450.1 /DEF=Homo sapiens bromodomain adjacent to zinc finger domain, 2B /DB_XREF=gi:7304922 /UG=Hs.8383 bromodomain adjacent to zinc finger domain, 2B /EL=gb:AB032255.1 gb:NM_013450.1
202558_s_at	gb:NM_006948.1 /DEF=Homo sapiens stress 70 protein chaperone, microsome-associated, 60kD /DB_XREF=gi:502125 /UG=Hs.288799 stress 70 protein chaperone, microsome-associated, 60kD /EL=gb:U04735.1 gb:NM_006948.1
201349_at	gb:NM_004152.1 /DEF=Homo sapiens solute carrier family 9 (sodiumhydrogen exchanger), isoform 3 regulatory factor 1 (SLC9A3R1), mRNA. /FEA=mRNA /GEN=SLC9A3R1 /PROD=solute carrier family 9 (sodiumhydrogen exchanger), isoform 3 regulatory factor 1 /DB_XREF=gi:4759139 /UG=Hs.184216 solute carrier family 9 (sodiumhydrogen exchanger), isoform 3 regulatory factor 1 /FL=gb:BC001443.1 gb:AF036241.1 gb:NM_004152.1
220603_s_at	gb:NM_018349.1 /DEF=Homo sapiens hypothetical protein FLJ11175 (FLJ11175), mRNA. /FEA=mRNA /GEN=FLJ11175 /PROD=hypothetical protein FLJ11175 /UG=Hs.33368 hypothetical protein FLJ11175 /EL=gb:NM_018349.1
35620_at	Cluster Incl. X62078: H.sapiens mRNA for GM2 activator protein /cds=UNKNOWN /gb=x62078 /gi=313158 /ug=Hs.69743 /len=2436
201731_s_at	gb:NM_003292.1 /DEF=Homo sapiens translocated promoter region (to activated MET oncogene) (TPR), mRNA. /FEA=mRNA /GEN=TTR /PROD=translocated promoter region (to activated MET oncogene) /EL=gb:NM_003292.1
202414_at	gb:NM_00123.1 /DEF=Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) (ERCC5), mRNA. /FEA=mRNA /GEN=ERCC5 /PROD=XP-G-complementing protein /DB_XREF=gi:1503600 /UG=Hs.48576 excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome)) /EL=gb:D16305.1 gb:L20046.1 gb:NM_000123.1
210422_x_at	gb:D50402.1 /DEF=Human mRNA for NRAMP1, complete cds. /FEA=mRNA /PROD=Nramp /DB_XREF=gi:1000996 /UG=Hs.182611 solute carrier protein 11 (oxoton-coupled divalent metal ion transporters), member 1 /EL=gb:D50402.1 gb:D50403.1
58890_at	Cluster Incl. AW025204:nu95h10.21 Homo sapiens cDNA, 3 end /clone=IMAGE-990806 /clone_end=3 /gb=AW025284 /gi=5878814 /ug=Hs.237946 /len=454
219890_at	gb:NM_012252.1 /DEF=Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA. /FEA=mRNA /GEN=CLECSF5 /PROD=C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 /DB_XREF=gi:10281668 /UG=Hs.126355 C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 /EL=gb:NM_013252.1 gb:AF139768.1
208112_x_at	gb:NM_006795.1 /DEF=Homo sapiens EH domain containing 1 (EH1), mRNA. /FEA=mRNA /GEN=EH1 /PROD=EH domain containing 1 /DB_XREF=gi:5003008 /UG=Hs.155119 EH domain containing 1 /EL=gb:AE09911.1 gb:NM_006795.1
218655_s_at	gb:NN_017748.1 /DEF=Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA. /FEA=mRNA /GEN=FLJ20291 /PROD=hypothetical protein FLJ20291 /DB_XREF=gi:8923270 /UG=Hs.8928 hypothetical protein FLJ20291 /EL=gb:NM_017748.1
214230_at	Consensus includes gb:R376664 /FEA=EST /DB_XREF=gi:795120 /DB_XREF=est:yf6le05.s1 /CLONE=IMAGE:26577 /UG=Hs.144409 cell division cycle 42 (GTP-binding protein, 25kDa)
201898_s_at	Consensus includes gb:AL126625 /FEA=EST /DB_XREF=gi:3598139 /DB_XREF=est:yg83a12.X1 /CLONE=IMAGE:1736062 /UG=Hs.80012 ubiquitin-conjugating enzyme E2A (RAD6 homolog) /EL=gb:NM_74524.1 gb:NM_003336.1

210773_s_at	gb:U81501.1 /DEF=Human lipoxin A4 receptor mRNA, complete cds. /FEA=mRNA /PROD=lipoxin A4 receptor /DB_XREF=gi:1916075 /UG=hs .908575 formyl peptide receptor-like 1 /EL=gb:M76672.1 qb:U81501.1 qb:AF054013.1
32069_at	Cluster Incl. AB014515:Homo sapiens mRNA for KIAA0615 protein, complete cds /cds=(237,2927) /gi=AB014515 /gi=3327043 /
121_at	ug=hs .155972 /len=3119
X69699 /FEATURE=	/DEFINITION=HSPAXXA H.sapiens Pax8 mRNA
202053_s_at	gb:J47162.1 /DEF=Human fatty aldehyde dehydrogenase (FALDH) mRNA, complete cds. /FEA=mRNA /GEN=FALDH /PROD=fatty aldehyde dehydrogenase /DB_XREF=gi:1082035 /UG=hs .159608 aldehyde dehydrogenase 3 family, member A2 /EL=gb:L47162.1
gb:U46669.1 qb:NM_000382.1	gb:NM_000382.1
212335_at	Consensus includes gb:AW167793 /FEA=EST /DB_XREF=gi:6399401 /DB_XREF=est:xg56d07.x1 /CLONE=IMAGE:2632333 /UG=hs .164036 Homo sapiens AKAP35C mRNA sequence, alternatively spliced
gb:NM_016768.1 /DEF=Human T-cell receptor gamma chain V _{GT} -C _{T1} -C _{T1} region mRNA, complete cds. /FEA=mRNA /GEN=TCRG /DB_XREF=gi:39339 /UG=hs .112259 T cell receptor gamma locus /EL=gb:NM_016768.1 qb:AF15103.1	
204717_at	gb:NM_001549.1 /DEF=Homo sapiens interferon-induced protein with tetrasericopeptide repeats 4 (TETRA4) mRNA, /FEA=mRNA /GEN=TETRA4 /PROD=tetrasericopeptide repeats 4 (TETRA4) mRNA /DB_XREF=gi:4504586 /UG=hs .181874 interferon-induced protein with tetrasericopeptide repeats 4 /EL=gb:BC001333.1 qb:BC001333.1 qb:U52513.1 qb:AF026939.1
gb:AF083470.1 qb:NM_001549.1	
212233_at	Consensus includes gb:AI926544 /FEA=EST /DB_XREF=gi:5662508 /DB_XREF=est:wo46cl2.x1 /CLONE=IMAGE:2458390 /UG=hs .303154 copeye protein 3
216890_at	Consensus includes gb:N36408 /FEA=EST /DB_XREF=gi:1157550 /DB_XREF=est:yy33f03.s1 /CLONE=IMAGE:273053 /UG=hs .325364 hypothetical protein ELJ23306 /EL=gb:NM_025530.1
202460_s_at	gb:NM_014646.1 /DEF=Homo sapiens lipin 2 (LIPIN2) mRNA. /FEA=mRNA /GEN=LIPIN2 /PROD=lipin 2 /DB_XREF=gi:7662021 /UG=hs .166318 lipin 2 /EL=gb:D81436.1 qb:NM_014646.1
58780_s_at	Cluster Incl. R42419:yg02a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-30331 /clone_end=3 /gi=817213 /ug=hs .25831 /len=31
205201_s_at	gb:NM_002641.1 /DEF=Homo sapiens phosphatidylinositol glycan, Class A (paroxysmal nocturnal hemoglobinuria) (PIGA), transcript variant 1, mRNA. /FEA=mRNA /GEN=PIGA /PROD=phosphatidylinositol glycan, class A Isoform 1 /DB_XREF=gi:11663129 /UG=hs .51 phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria) /EL=gb:NM_002641.1 qb:DI1466.1
218231_at	gb:NM_021242.1 /DEF=Homo sapiens hypothetical protein STRAIT1499 (STRAIT1499) mRNA, /FEA=mRNA /GEN=STRAIT1499 /PROD=Hypothetical protein STRAIT1499 /DB_XREF=gi:10884050 /UG=hs .236556 hypothetical protein STRAIT1499 /EL=gb:NM_021242.1
212491_s_at	Consensus includes gb:AI121061 /FEA=EST /DB_XREF=gi:3777662 /DB_XREF=est:sp29el0.x1 /CLONE=IMAGE:1956787 /UG=hs .250641 tropomyosin 4
213202_s_at	Consensus includes gb:AI908770 /FEA=EST /DB_XREF=gi:3048175 /DB_XREF=est:oi06ai1.s1 /CLONE=IMAGE:1522652 /UG=hs .283881 KRA0013 protein
221497_x_at	gb:BC005369.1 /DEF=Homo sapiens, chromosome 1 open reading frame 12, clone MGC:12484 mRNA, complete cds. /FEA=mRNA /PROD=chromosome 1 open reading frame 12 /DB_XREF=gi:113529208 /UG=hs .6523 chromosome 1 open reading frame 12 /EL=gb:AF229245.1 qb:AE277116.1 qb:NM_022051.1 qb:BC005369.1
212185_x_at	Consensus includes gb:NM_005953.1 /DEF=Homo sapiens metallothionein 2A (MT2A) mRNA. /FEA=mRNA /GEN=MT2A /PROD=metallothionein 2A /DB_XREF=gi:5174763 /UG=hs .118786 metallothionein 2A /EL=gb:NM_005953.1
203961_at	Consensus includes gb:AI157398 /DEF=Human DNA sequence from clone RP1-56f17 on chromosome 10. Contains ESTs, STSs and GSSs. Contains the gene for the nebulette protein (NEBL, actin-binding z-disc protein) /FEA=mRNA_1 /DB_XREF=gi:10045326 /UG=hs .5025 nebulette /EL=gb:NM_006393.1
210966_s_at	gb:Z224727.1 /DEF=H.sapiens tropomyosin isoform mRNA, complete CDS. /FEA=mRNA /PROD=tropomyosin isoform /DB_XREF=gi:894188 /UG=hs .77899 tropomyosin 1 (alpha) /EL=gb:G24727.1
41386_i_at	Cluster Incl. AB002344:Human mRNA for KIAA0346 gene, partial cds /cds=(0,4852) /gb=AB002344 /gi=2280479 /ug=hs .103915 /len=6121
201874_at	Consensus includes gb:BF978611 /FEA=EST /DB_XREF=gi:12345826 /DB_XREF=est:602149061FL /CLONE=IMAGE:4307822 /UG=hs .14891 hypothetical protein ELJ21047 /EL=gb:NM_0245569.1
211781_x_at	gb:BC006164.1 /DEF=Homo sapiens, clone MGC:13219, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for NGC:113219) /DB_XREF=gi:113544062 /EL=gb:BC006164.1
202459_s_at	Consensus includes gb:U55968 /FEA=EST /DB_XREF=gi:13354524 /DB_XREF=est:HSU55968 /CLONE=26508 /UG=hs .166318 Lipin 2 /EL=gb:DB71436.1 qb:NM_014646.1

201195_s_at	gb:AB018009.1 /DEF=Homo sapiens mRNA for L-type amino acid transporter 1, complete cds. /FEA=mRNA /GEN=NLAT1 /PROD=L-type amino acid transporter 1 /DB_XREF=gi:5926731 /UG=Rs.1B4601 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 /FT=gb;AF018542.1 gb:BR018542.1 gb:AF04032.1 gb:NM_003486.1 gb:BB017908.1 gb:AB018009.1
217918_at	gb:NM_014183.1 /DEF=Homo sapiens HSPC162 protein (HSPC162), mRNA. /FEA=mRNA /GEN=HSPC162 /PROD=HSPC162 protein /DB_XREF=gi:1661821 /UG=Rs.100002 HSPC162 protein /FT=gb;BC002481.1 gb:AY026513.1 gb:AF161511.1 gb:NM_014183.1 gb:AF165516.1

Tabelle 4: Gene aus Clusteranalyse 4

Affymetrix interne Bezeichnung	Beschreibung der Sequenz in der Genebank Datenbank
221798_x_at	Consensus includes gb:AI183766 /FEA=EST /DB_XREF=gi:3734404 /DB_XREF=est:gi17q06.x1 /CLONE=IMAGE:1739290 /UG=Hs.182426
218231_at	Consensus includes N-Acetylglucosamine kinase (HSA242910), mRNA. /FEA=mRNA /GEN=HSA242910 /PROD=N-ribosomal protein S2
201009_s_at	Acetylglucosamine kinase /DB_XREF=gi:8923736 /UG=Hs.7036 N-Acetylglucosamine kinase /FL=gb:BC001029.1 gb:NM_017567.1 Consensus includes gb:AI439356 /FEA=EST /DB_XREF=gi:4305149 /DB_XREF=est:tc90c12.x1 /CLONE=IMAGE:2073310 /UG=Hs.179526 upregulated
212998_x_at	Consensus includes gb:AI583173 /FEA=EST /DB_XREF=est:gi:4569070 /DB_XREF=est:tq64e04.x1 /CLONE=IMAGE:2213598 /UG=Hs.73931 major histocompatibility complex, class II, DQ beta 1
201464_x_at	Consensus includes gb:BG491844 /FEA=EST /DB_XREF=gi:13453356 /DB_XREF=est:602535931T1 /CLONE=IMAGE:4684998 /UG=Hs.78465 v-jun avian sarcoma virus 17 oncogene homolog /FL=gb:BC002616.1 gb:NM_002228.2
214687_x_at	Consensus includes gb:AK025577.1 /DEF=Homo sapiens cDNA: FLJ2924 fis, clone KAT06977, highly similar to HSALDAR Human fibroblast mRNA for aldolase A. /FEA=mRNA /DB_XREF=gi:10439461 /UG=Hs.273415 aldolase A, fructose-bisphosphate
220532_s_at	gb:NM_04020.1 /DEF=Homo sapiens LR8 protein (LR8), mRNA. /FEA=mRNA /GEN=LR8 /PROD=LR8 protein /DB_XREF=gi:7662497 /UG=Hs.190161
205987_at	LR8 protein /FL=gb:AF115384.1 gb:NM_014020.1 gb:NM_001765.1 /DEF=Homo sapiens CD1C antigen, c polypeptide (CD1C), mRNA. /FEA=mRNA /GEN=CD1C /PROD=CD1C antigen, c polypeptide /DB_XREF=gi:4502646 /UG=Hs.1311 CD1C antigen, c polypeptide /FL=gb:M28827.1 gb:NM_001765.1
202658_at	.1 /DEF=Homo sapiens peroxisomal biogenesis factor 11B (PEX11B), mRNA. /GEN=PEX11B /PROD=peroxisomal biogenesis factor 11B /DB_XREF=gi:4503718 /UG=Hs.83023 peroxisomal biogenesis factor 11B /FL=gb:AF093670.1 gb:AB018080.1 gb:NM_003846.1
200991_s_at	gb:NM_014748.1 /DEF=Homo sapiens KIAA0064 gene product (KIAA0064), mRNA. /FEA=mRNA /GEN=KIAA0064 /PROD=KIAA0064 gene product /DB_XREF=gi:7661889 /UG=Hs.278569 sorting nexin 17 /FL=gb:BC002524.1 gb:BC002610.1 gb:NM_014748.1
209007_s_at	gb:AF267856.1 /DEF=Homo sapiens HT033 mRNA, complete cds. /FEA=mRNA /PROD=HT033 /DB_XREF=gi:12006038 /UG=Hs.8084 hypothetical Protein dj465N24.2.1 /FL=gb:AF247168.1 gb:AF267856.1
213969_x_at	Consensus includes gb:BF683426 /FEA=EST /DB_XREF=gi:11968834 /DB_XREF=est:602139603F1 /CLONE=IMAGE:4300777 /UG=Hs.183698 ribosomal protein L29
200094_s_at	Consensus includes gb:AI004246 /FEA=EST /DB_XREF=gi:3213756 /DB_XREF=est:cu03g06.x1 /CLONE=IMAGE:1625242 /UG=Hs.75309 eukaryotic translation elongation factor 2
208929_x_at	gb:BC004954.1 /DEF=Homo sapiens, clone NGC:10897, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10897) /DB_XREF=gi:13436331 /UG=Hs.180842 ribosomal protein L13 /FL=gb:BC004954.1 gb:NM_000977.1

206170_at	gb:NM_000024.2 /DEF=Homo sapiens adrenergic, beta-2-, receptor, surface (ADRB2), mRNA. /FEA=mRNA /GEN=ADRB2
/PROD=adrenergic, beta-2-, receptor, surface /DB_XREF=gi:131162366 /UG=Hs_2551 adrenergic, beta-2-, receptor, surface /FI=gb:NM_000024.2 qb:MI15169.1	
Consensus includes gb:AL04923.1 /DEF=Homo sapiens mRNA; cDNA DKFZP564E2282 (from clone DKFZP564E2282). /FEA=mRNA	
/DB_XREF=gi:4884169 /UG=Hs_KIAA1451 protein	
212582_at	Consensus includes gb:AI972144 /FEA=EST /DB_XREF=gi:5768970 /DB_XREF=est:wr63b03.x1 /CLONE=IMAGE:2492333
/UG=Hs_75860 hydroxacyl-Coenzyme A dehydrogenase3-ketoacyl-Coenzyme A thiolaseenoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit /FI=gb:NM_000182.1 qb:D16480.1 qb:U04627.1	
208630_at	Consensus includes gb:AI972144 /FEA=EST /DB_XREF=gi:5768970 /DB_XREF=est:wr63b03.x1 /CLONE=IMAGE:2492333
/UG=Hs_92137 v-myc protein gene, complete cds /FEA=mRNA_2 /DB_XREF=gi:1888906	
214058_at	Consensus includes gb:BF223224 /FEA=EST /DB_XREF=gi:11130401 /DB_XREF=est:7q30g05.x1 /CLONE=IMAGE:3700017
/UG=Hs_92137 v-myc avian myelocytomatosis viral oncogene homolog 1, lung carcinoma derived	
201991_s_at	Consensus includes gb:BF223224 /FEA=EST /DB_XREF=est:7q30g05.x1 /CLONE=IMAGE:3700017
/UG=Hs_149436 kinase family member 5B /FI=gb:NM_004321.1	
212179_at	Consensus includes gb:AV157501 /FEA=EST /DB_XREF=gi:6228902 /DB_XREF=est:au83a02.x1 /CLONE=IMAGE:2782826
/UG=Hs_18368 DKFZP564B0769 protein	
210949_s_at	gb:BC000533.1 /DEF=Homo sapiens, Similar to eukaryotic translation initiation factor 3, subunit 8 (110kD), clone MGC:8693,
mRNA, complete cds. /FEA=mRNA /PROD=Similar to eukaryotic translation initiation factor 3, subunit 8 (110kD)	
/DB_XREF=gi:12653522 /UG=Hs_4835 eukaryotic translation initiation factor 3, subunit 8 (110kD) /FI=gb:BC000533.1	
213142_x_at	Consensus includes gb:AV700415 /FEA=EST /DB_XREF=gi:10302386 /DB_XREF=est:AV700415 /CLONE=GKCDGA04 /UG=Hs_12969 hypothesical protein
217617_at	Consensus includes gb:BEB891920 /FEA=EST /DB_XREF=gi:10351728 /DB_XREF=est:601435490f1 /CLONE=IMAGE:3920590
/UG=Hs_323342 actin related protein 23 complex, subunit 4 (20 kD) /FI=gb:AF006087.1 qb:NM_005718.1	
216041_x_at	Consensus includes gb:AK023348.1 /DEF=Homo sapiens cDNA FLJ13286 fis, clone OVARC1001154, highly similar to Homo sapiens clone 24720 epithelin 1 and 2 mRNA.
202687_s_at	gb:U5059.1 /DEF=Homo sapiens Apo-2 ligand mRNA, complete cds. /FEA=mRNA /PROD=Apo-2 ligand /DB_XREF=gi:1336207
/UG=Hs_83429 tumor necrosis factor (ligand) superfamily, member 10 /FI=gb:U37518.1 qb:U37059.1 qb:NM_003810.1	
215230_x_at	Consensus includes gb:AA679705 /FEA=EST /DB_XREF=gi:2660227 /DB_XREF=est:ah15e04.s1 /CLONE=IMAGE:1156734
/UG=Hs_4835 eukaryotic translation initiation factor 3, subunit 8 (110kD)	
200647_x_at	gb:NM_003752.2 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110kD) /DB_XREF=gi:5579457
/FEA=mRNA /GEN=EIF3S8 /PROD=eukaryotic translation initiation factor 3, subunit 8 (110kD) /FI=gb:NM_003752.2	
200078_s_at	gb:BC005876.1 /DEF=Homo sapiens, ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 21kD, clone MGCG4498, mRNA, complete cds. /FEA=mRNA /PROD=ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 21kD /DB_XREF=gi:13543337
/FL=gb:BC005876.1	
202169_s_at	gb:AF02110.1 /DEF=Homo sapiens alpha-amino adipic semialdehyde dehydrogenase-phosphopantetheinyl transferase mRNA, complete cds. /FEA=mRNA /PROD=alpha-amino adipic semialdehyde dehydrogenase-phosphopantetheinyl transferase /DB_XREF=gi:1112034 /UG=Hs_64595 amino adipate dehydrogenase-phosphopantetheinyl transferase /FI=gb:AF302110.1 qb:AF136978.1 qb:AF151057.1 qb:NM_015423.1 qb:AF201913.1
202659_at	gb:NM_002801.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, beta type, 10 (PSMB10), mRNA. /GEN=PSMB10 /PROD=proteasome (prosome, macropain) subunit, beta type, 10 /DB_XREF=gi:14506190 /UG=Hs_9661 proteasome (prosome, macropain) subunit, beta type, 10 /FI=gb:NM_002801.1
221488_s_at	gb:AF230924.1 /DEF=Homo sapiens brain acetylcholinesterase putative membrane anchor mRNA, complete cds. /FEA=mRNA /PROD=brain acetylcholinesterase putative membrane anchor /DB_XREF=gi:7341254 /UG=Hs_107187 divalent cation tolerant protein CUTA /FI=gb:AF230924.1
221622_s_at	gb:AF246240.1 /DEF=Homo sapiens HT026 mRNA, complete cds. /FEA=mRNA /PROD=HT026 /DB_XREF=gi:12005514
/UG=Hs_24371 uncharacterized hypothalamus protein HT007 /FI=gb:AF246240.1	

206050_s_at	gb:NM_002939.1 /DEF=Homo sapiens ribonucleaseangiogenin inhibitor (RNH) , mRNA. /FEA=mRNA /GEN=rnh /PROD=ribonucleaseangiogenin inhibitor /DB XREF=gi:1506564 /UG=Hs .75108 ribonucleaseangiogenin inhibitor /FL=gb:M36717.1 gb:NM_002939.1
212199_at	Consensus includes gb:AI566962 /DEF=EST /DB XREF=gi:129919867 /DB_XREF=est:AI566962 /CLONE=c50DF026YH08 (3 prime) /UG=Hs .284281 Human putative ribosomal protein S1 mRNA
201861_s_at	Consensus includes gb:BR965566 /DEF=EST /DB XREF=gi:12332781 /DB_XREF=est:60227032F1 /CLONE=IMAGE:4364790 /UG=Hs .326159 leucine rich repeat (in FLII) interacting protein 1 /FL=gb:NM_004735.1
212795_at	Consensus includes gb:AI137753.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434K1412 (from clone DKFZp434K1412) . /FEA=mRNA /DB XREF=gi:6808455 /UG=Hs 12144 KIAA1033 protein
213574_s_at	Consensus includes gb:AA8861608 /DEF=EST /DB XREF=gi:2953748 /DB_XREF=est:ak34e01.s1 /CLONE=IMAGE:1407864 /UG=Hs .180446 karyopherin (importin) beta 1
215171_s_at	Consensus includes gb:AK023063.1 /DEF=Homo sapiens cDNA FLJ13001 fis, clone NT2RP3000341, highly similar to Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein. /FEA=mRNA /DB XREF=gi:10434808 /UG=Hs .20716 translocase of inner mitochondrial membrane 17 (yeast) homolog A
210137_s_at	gb:BC001286.1 /DEF=Homo sapiens, Similar to dCMP deaminase, Clone MGC-5160, mRNA, complete cds. /FEA=mRNA /PROD=Similar to dCMP deaminase /DB XREF=gi:12651884 /UG=Hs .76894 dCMP deaminase /FL=gb:BC001286.1
212943_at	Consensus includes gb:AB011100.2 /DEF=Homo sapiens mRNA for KIAA0528 protein, partial cds. /FEA=mRNA /GEN=KIAA0528 /PROD=KIAA0528 protein /DB XREF=gi:6883714 /UG=Hs .30656 KIAA0528 gene product
202164_s_at	gb:AF180476.1 /DEF=Homo sapiens CALIF (CALIF) mRNA, complete cds. /FEA=mRNA /GEN=CALIF /PROD=CALIFP /DB_XREF=gi:68856208 /UG=Hs .26703 CCR4-NOT transcription complex, subunit 8 /FL=gb:AF053318.1 gb:NM_004779.1 gb:AF180476.1
209005_at	gb:AF157333.1 /DEF=Homo sapiens P45SXP2-like protein mRNA, complete cds. /FEA=mRNA /PROD=P45SXP2-like Protein /DB XREF=gi:7688996 /UG=Hs .55548 f-box and leucine-rich repeat protein 5 /FL=gb:AF199420.1 gb:AF142481.1 gb:AF157323.1
202899_s_at	gb:NM_003017.1 /DEF=Homo sapiens splicing factor, argininoserine-rich 3 (SFRS3) , mRNA. /FEA=mRNA /GEN=SFRS3 /PROD=splicing factor, argininoserine-rich 3 /DB_XREF=gi:4506900 /UG=Hs .167460 splicing factor, argininoserine-rich 3 /FL=gb:L0838.1 gb:NM_003017.1
208777_s_at	gb:AF001212.1 /DEF=Homo sapiens 26S Proteasome subunit 9 mRNA, complete cds. /FEA=mRNA /PROD=26S Proteasome subunit 9 /DB_XREF=gi:2150045 /UG=Hs .90744 proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 /FL=gb:BC004437.1 gb:BC004430.1 gb:AB003102.1 gb:AF001212.1 gb:NM_002815.1
219889_at	gb:NM_005479.1 /DEF=Homo sapiens frequently rearranged in advanced T-cell lymphomas (FRAT1) , mRNA. /FEA=mRNA /GEN=FRAT1 /PROD=frequently rearranged in advanced T-cell lymphomas /DB_XREF=gi:4885246 /UG=Hs .126057 frequently rearranged in advanced T-cell lymphomas /FL=gb:US8975.2 gb:NM_005479.1
204961_s_at	gb:NM_000265.1 /DEF=Homo sapiens neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1) (NCF1) , mRNA. /FEA=mRNA /GEN=NCF1 /PROD=neutrophil cytosolic factor 1 /DB_XREF=gi:4557784 /UG=Hs .1583 neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1) /FL=gb:BC002816.1 gb:AF330627.1 gb:M55067.1 gb:NM_000265.1
217106_x_at	Consensus includes gb:AF091078.1 /DEF=Homo sapiens clone 559 unknown mRNA, complete sequence. /FEA=mRNA /PROD=unknown /DB_XREF=gi:3559993 /UG=Hs .125819 putative dimethyladenosine transferase
212224_at	Consensus gb:NM_000689.1 /DEF=Homo sapiens aldehyde dehydrogenase 1, soluble /DB_XREF=gi:4502030 /UG=Hs .76392 aldehyde dehydrogenase 1 family, member A1 /FL=gb:AE003341.1 gb:NM_000689.1
204125_at	gb:NM_016013.1 /DEF=Homo sapiens CGI-65 protein (LOC51103) , mRNA. /FEA=mRNA /GEN=LOC51103 /PROD=CGI-65 Protein /DB_XREF=gi:7705778 /UG=Hs .106529 CGI-65 protein /FL=gb:BC000780.1 gb:AF151823.1 gb:NM_016013.1
217752_s_at	gb:NM_018235.1 /DEF=Homo sapiens hypothetical protein FLJ10830 (FLJ10830) , mRNA. /FEA=mRNA /GEN=FLJ10830 /PROD=hypothetical protein FLJ10830 /DB_XREF=gi:9922698 /UG=Hs .273230 hypothetical protein FLJ10830 /FL=gb:BC001375.1 gb:NM_018235.1
221087_s_at	gb:NM_014349.1 /DEF=Homo sapiens apolipoprotein L, 3 (APOL3) , mRNA. /FEA=mRNA /GEN=APOL3 /PROD=apolipoprotein L, 3

	/DB_XREF=gi:7656972 /UG=Hs_241535 apolipoprotein L, 3 /FL=gb:AY014905.1 gb:AF070675.1 gb:NM_014349.1
218139_s_at	gb:NM_018229.1 /DEF=Homo sapiens hypothetical protein FLJ10813 (FLJ10813), mRNA. /FEA=mRNA /GEN=FLJ10813 /PROD=hypothetical protein FLJ10813 /DB_XREF=gi:8922687 /UG=Hs_106210 hypothetical protein FLJ10813 /FL=gb:AL136695.1 gb:NM_012229.1
213878_at	Consensus includes gb:AI68944 /FEA=EST /DB_XREF=gi:4897238 /DB_XREF=est:tu38g02_x1 /CLONE=IMAGE:2253362 /UG=Hs_235069 RecQLike (DNA helicase QL-like)
201346_at	gb:NM_024551.1 /DEF=Homo sapiens hypothetical protein FLJ21432 (FLJ21432), mRNA. /FEA=mRNA /GEN=FLJ21432 /PROD=hypothetical protein FLJ21432 /DB_XREF=gi:13337514 /UG=Hs_11641 hypothetical protein FLJ21432 /FL=gb:NM_024551.1 gb:BC004906.1
206874_s_at	Consensus includes gb:AL137761 /DEF=Human DNA sequence from clone RP11-16H23 on chromosome 10. Contains the gene KIAA0204 (HSLK) for a protein kinase, the COL17A1 gene for collagen type XVII alpha 1 (BP180), ESTs and GSSs /FEA=mRNA_2 /DB_XREF=gi:8573811 /UG=Hs_105751 Ste20-related serine/threonine kinase /FL=gb:D86959.1 gb:NM_014720.1
221808_at	Consensus includes gb:NM_004251.1 /DEF=Homo sapiens RAB9, member RAS oncogene family (RAB9), mRNA. /FEA=CDS /GEN=RAB9 /PROD=RAB9, member RAS oncogene family /DB_XREF=gi:4759011 /UG=Hs_28726 RAB9, member RAS oncogene family /FL=gb:U444103.1 gb:NM_004251.1
211138_s_at	gb:BC005297.1 /DEF=Homo sapiens, Similar to kynurenine 3-monoxygenase (kynurenine 3-hydroxylase), clone MGC:123362, mRNA, complete cds. /FEA=mRNA /PROD=Similar to kynurenine 3-monoxygenase (kynurenine 3-hydroxylase) /DB_XREF=gi:13529016 /UG=Hs_107318 kynurenine 3-monoxygenase (kynurenine 3-hydroxylase) /FL=gb:BC005297.1
201386_s_at	gb:AF279891.1 /DEF=Homo sapiens dead box protein 15 mRNA, complete cds. /FEA=mRNA /PROD=dead box protein 15 /DB_XREF=gi:9524452 /UG=Hs_5683 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 15 /FL=gb:AB001636.1 gb:NM_001358.1
203037_s_at	gb:NM_014751.1 /DEF=Homo sapiens KIAA0429 gene product (KIAA0429), mRNA. /FEA=mRNA /PROD=KIAA0429 gene product /DB_XREF=gi:7662113 /UG=Hs_77694 KIAA0429 gene product /FL=gb:AB007889.1 gb:NM_014751.1
218356_at	gb:NM_013393.1 /DEF=Homo sapiens cell division protein FtsJ (FTH1), mRNA. /FEA=mRNA /PROD=cell division protein FtsJ /DB_XREF=gi:7019376 /UG=Hs_279877 cell division protein FtsJ /FL=gb:AF093415.1 gb:NM_01393.1
204405_x_at	gb:NM_014473.1 /DEF=Homo sapiens putative dimethyladenosine transferase (HSA9761), mRNA. /FEA=mRNA /GEN=HSA9761 /PROD=putative dimethyladenosine transferase /DB_XREF=gi:7657197 /UG=Hs_125819 putative dimethyladenosine transferase /FL=gb:AE102147.1 gb:NM_014473.1
201608_s_at	gb:NM_007062.1 /DEF=Homo sapiens nuclear phosphoprotein similar to S. cerevisiae PWP1 (PWP1), mRNA. /FEA=mRNA /GEN=PWP1 /PROD=nuclear phosphoprotein similar to S. cerevisiae PWP1 /DB_XREF=gi:5502033 /UG=Hs_172589 nuclear phosphoprotein similar to S. cerevisiae PWP1 /FL=gb:BC001652.1 gb:NM_007062.1
201569_s_at	gb:NM_015380.1 /DEF=Homo sapiens CGI-51 protein (CGI-51), mRNA. /FEA=mRNA /GEN=CGI-51 /PROD=CGI-51 protein /DB_XREF=gi:1661541 /UG=Hs_4877 CGI-51 protein /FL=gb:AF151809.1 gb:NM_015380.1
222244_s_at	Consensus includes gb:AK000749.1 /DEF=Homo sapiens cDNA FLJ20742 fis, clone HEP06891. /FEA=mRNA /DB_XREF=gi:7021031 /UG=Hs_52184 hypothetical protein FLJ20618
201241_at	gb:NM_004939.1 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1 /DB_XREF=gi:4626685 /UG=Hs_78580 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1 /PROD=DEADH (Asp-Glu-Ala-AspHis) /FL=gb:X70649.1 gb:NM_004939.1
220731_s_at	gb:NM_01090.1 /DEF=Homo sapiens hypothetical protein FLJ10420 (FLJ10420), mRNA. /FEA=mRNA /GEN=FLJ10420 /PROD=hypothetical protein FLJ10420 /DB_XREF=gi:8922415 /UG=Hs_289087 hypothetical protein FLJ10420 /FL=gb:NM_010809.1
208739_at	gb:BC004146.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, beta type, 5, clone MGC:2175, mRNA, complete cds.

	/FEA=mRNA /PROD=proteasome (prosome, macropain) subunit, betatype, 5 /FL=gb:BC004146.1 gb:NM 002797.1 gb:D29011.1 (prosome, macropain) subunit, beta type, 5 /FL=gb:BC004146.1 gb:NM 002797.1 gb:D29011.1
221718_s_at	gb:M90360.1 /DEF=Human type II cAMP-dependent protein kinase (Ht31) mRNA, complete cds. /FEA=CDS /GEN=Ht31 /PROD=protein kinase /DB_XREF=gi:184434 /FL=gb:M90360.1
208662_s_at	Consensus includes gb:AI865338 /DB_XREF=gi:5590502 /DB_XREF=est:w192e09.x1 /CLONE=IMAGE:2432392 /UG=Hs_118174 tetratricopeptide repeat domain 3 /FL=gb:D84294.1
202118_s_at	Consensus includes gb:AA541758 /DB_XREF=gi:2288192 /DB_XREF=est:n187d05.s1 /CLONE=IMAGE:983817 /UG=Hs_14158 copine III /FL=gb:AB014536.1 gb:NM 003969.1 gb:AF077226.2
201740_at	gb:NM 0045551.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) (NDUF53), mRNA. /FEA=mRNA /GEN=NDUF53 /PROD=NDUF53 /DB_XREF=gi:2540827 /DB_XREF=est:af26502.s1 /CLONE=IMAGE:1032795 /DB_XREF=gi:4758787 /UG=Hs_5273 NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) /FL=gb:BC00617.1 gb:AF067139.1 gb:NM 004551.1 gb:AF10743.1
215952_s_at	Consensus includes gb:AF090094.1 /DEF=Homo sapiens clone IMAGE 172979. /FEA=mRNA /DB_XREF=gi:4063629 /UG=Hs_125078 ornithine decarboxylase antizyme 1
212796_s_at	Consensus includes gb:BF195608 /DB_XREF=gi:11082676 /DB_XREF=est:7n85503.x1 /CLONE=IMAGE:3571349 /UG=Hs_126084 KIAA01055 protein
210561_s_at	gb:AL110243.1 /DEF=Homo sapiens mRNA; cDNA DKTZP56450482 (from clone DKTZP56450482); complete cds. /FEA=mRNA /GEN=DKEZP56450482 /PROD=hypothetical protein /DB_XREF=gi:5817189 /UG=Hs_187991 DKEZP56450482 protein /FL=gb:AF072880.1 gb:AF106683.1 gb:AL110243.1 gb:AF112205.1 gb:AF169313.2
202220_at	gb:NM 014949.1 /DEF=Homo sapiens KIAA0907 protein (KIAA0907). mRNA. /FEA=mRNA /GEN=KIAA0907 /PROD=KIAA0907 protein /DB_XREF=gi:7662371 /UG=Hs_24656 KIAA0907 protein /FL=gb:AB020714.1 gb:NM 014949.1
203739_at	gb:NM_006526.1 /DEF=Homo sapiens zinc finger protein 217 (2NF217), mRNA. /FEA=mRNA /GEN=ZNF217 /PROD=zinc finger protein 217 /DB_XREF=gi:5730123 /UG=Hs_155040 zinc finger protein 217 /FL=gb:AF041259.1 gb:NM 005526.1
211036_x_at	gb:BC006301.1 /DEF=Homo sapiens anaphase-promoting complex subunit 5 /DB_XREF=gi:13623410 /FL=gb:BC006301.1 /PROD=anaphase-promoting complex subunit 5, clone MGC:132955, mRNA, complete cds. /FEA=mRNA
204060_s_at	gb:NM 005044.1 /DEF=Homo sapiens protein kinase, X-linked (PRKX), mRNA. /FEA=mRNA /GEN=PRKX /PROD=protein kinase, X-linked /DB_XREF=gi:4826947 /UG=Hs_147996 protein kinase, X-linked /FL=gb:NM 005044.1
64049_at	Cluster Incl. AI435089:ch95b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE:2126397 /clone_end=3 /gb:gi:AI435089 /gi:4300737 /ug=Hs_26194 /len=891
201515_s_at	gb:NM_04622.1 /DEF=Homo sapiens translin (TSN), mRNA. /FEA=mRNA /GEN=TSN /PROD=translin /DB_XREF=gi:4759269 /UG=Hs_750666 translin /FL=gb:NM 004622.1
219093_at	gb:NM_017933.1 /DEF=Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /FEA=mRNA /GEN=FLJ20701 /PROD=hypothetical protein FLJ20701 /DB_XREF=gi:8923631 /UG=Hs_169764 hypothetical protein FLJ20701 /FL=gb:NM 017933.1
221739_at	Consensus includes gb:AI524093 /FEA=EST /DB_XREF=gi:12787586 /DB_XREF=est:AL524093 /CLONE=CSODC002X104 (5 prime) /UG=Hs_10927 hypothetical protein EUROMAGE1875335
208622_s_at	gb:U18321.1 /DEF=human ionizing radiation resistance conferring protein mRNA, complete cds. /FEA=mRNA /PROD=ionizing radiation resistance conferring protein /DB_XREF=gi:603763 /UG=Hs_159627 death associated protein 3 /FL=gb:U18321.1 gb:NM_014222.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV) (NDUF53), mRNA. /FEA=mRNA /GEN=NDUF53 /PROD=NDUF53 /DB_XREF=gi:7657368 /UG=Hs_31547 NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 8 (19kD, PGIV) /DB_XREF=gi:AF044953.1 gb:NM 014222.1
221728_x_at	Consensus includes gb:AA628440 /FEA=EST /DB_XREF=gi:2540827 /DB_XREF=est:af26502.s1 /CLONE=IMAGE:1032795 /UG=Hs_83623 nuclear receptor subfamily 1, group I, member 3

210943_s_at	gb:U84744.1 /DEF=Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds. /FEA=mRNA /GEN=LYST /FL=gb:U84744.1 /PROD=Chediak-Higashi syndrome protein short isoform /DB_XREF=gi:2654473 /UG=Hs .36508 Chediak-Higashi syndrome 1
209104_s_at	gb:BC00009.1 /DEF=Homo sapiens, likely homolog of yeast Nhp2, component of the HACA snRNP; hypothetical protein FLJ20479, clone MCC:1038, mRNA, complete cds. /FEA=mRNA /PROD=likely homolog of yeast Nhp2, component of the HACA snRNP; hypothetical protein FLJ20479 /DB_XREF=gi:12632540 /UG=Hs .23990 nucleolar protein family A, member 2 (HACA small nucleolar RNPs) /FL=gb:BC00009.1 gb:NM_017838.1
217987_at	gb:NM_019048.1 /DEF=Homo sapiens hypothetical protein (FLJ20752), mRNA. /FEA=mRNA /GEN=FLJ20752 /PROD=hypothetical protein /DB_XREF=gi:9506696 /UG=Hs .101364 hypothetical protein (prosome, macropain) 26S subunit, ATPase, 6 (PSMC6), mRNA. /FEA=mRNA /GEN=FSCC6 /PROD=proteasome (prosome, macropain) 26S subunit,ATPase, 6 /DB_XREF=gi:4506214 /UG=Hs .79357 proteasome (prosome, macropain) 26S subunit, ATPase, 6 /FL=gb:BC005390.1 gb:D78275.1 gb:AF006305.1 gb:NM_002806.1
201699_at	gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FEA=mRNA /GEN=COPB /PROD=coatomer protein complex, subunit beta (COPB), mRNA. /FL=gb:AF084457.1 gb:AL136593.1 gb:NM_016451.1
210027_s_at	gb:M80267.1 /DEF=Human apurinic endonuclease (APE) mRNA, complete cds. /FEA=mRNA /GEN=APE /PROD=apurinic endonuclease /DB_XREF=gi:178742 /UG=Hs .73722 APEX nuclelease (multifunctional DNA repair enzyme) /FL=gb:BC004979.1 gb:NM_00267.1
202096_s_at	gb:NM_000714.2 /DEF=Homo sapiens benzodiazapine receptor (peripheral) (BZRP), nuclear gene encoding mitochondrial protein, transcript variant PBR, mRNA. /FEA=mRNA /GEN=BZRP /PROD=peripheral benzodiazapine receptor /DB_XREF=gi:6382068 /UG=Hs .202 benzodiazapine receptor (peripheral) /FL=gb:BC001110.1 gb:M3605.1 gb:NM_000714.2
214948_s_at	Consensus includes gb:AL051336.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141) /FEA=mRNA /DB_XREF=gi:4884446 /UG=Hs .140945 Homo sapiens mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141)
200042_at	gb:NM_014306.1 /DEF=Homo sapiens hypothetical protein (HSPC117), mRNA. /FEA=mRNA /GEN=HSPC117 /PROD=similar to C. elegans hypothetical 55.2 kd protein FL6A11.2 /DB_XREF=gi:7657014 /UG=Hs .10729 hypothetical protein /FL=gb:BC000151.1 gb:BC002970.1 gb:AF161466.1 gb:NM_014306.1 gb:AF155658.1.
219035_s_at	gb:NM_05126.1 /DEF=Homo sapiens hypothetical protein FLJ21786 (FLJ21786), mRNA. /FEA=mRNA /GEN=FLJ21786 /PROD=hypothetical protein FLJ21786 /DB_XREF=gi:13376704 /UG=Hs .316809 hypothetical protein FLJ21786 /FL=gb:NM_025126.1
200041_s_at	gb:NM_004640.1 /DEF=Homo sapiens HLA-B associated transcript-1 (D6S81E), mRNA. /FEA=mRNA /GEN=D6S81E /PROD=HLA-B associated transcript-1 /DB_XREF=gi:4758111 /UG=Hs .55296 HLA-B associated transcript-1 /FL=gb:BC004350.1 gb:NM_004640.1
216321_s_at	Consensus includes gb:X03338.1 /DEF=Human mRNA for beta-glucocorticoid receptor (clone OB10). /FEA=mRNA /PROD=beta-glucocorticoid receptor subfamily 3, group C, member 1
214574_x_at	Consensus includes gb:NM_007161.1 /DEF=Homo sapiens DNA segment on chromosome 6 (unique) 49 expressed sequence, NK cell triggering receptor, p30 (D6S49E), mRNA. /FEA=CDS /GEN=D6S49E /PROD=leukocyte-specific transcript 1 /DB_XREF=gi:6005740 /UG=Hs .88411 lymphocyte antigen 117 /FL=gb:NM_007161.1
205370_x_at	gb:NM_001918.1 /DEF=Homo sapiens dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) (DBT), mRNA. /FEA=mRNA /GEN=DBT /PROD=dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) /DB_XREF=gi:450364 /UG=Hs .139410 dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) /FL=gb:J03208.1 gb:NM_001918.1 gb:NM_001918.1 gb:NM_001918.1
2136872_at	Consensus includes gb:BE465032 /FEA=EST /DB_XREF=est:hv76g09.x1 /CLONE=hv76g09.x1 /IMAGE:3179392

	/UG=Hs.173685 hypothetical protein FLJ12619
201576_s_at	gb:NM_000404.1 /DEF=Homo sapiens galactosidase, beta 1 (GB1), mRNA. /FEA=mRNA /GEN=GB1 /PROD=galactosidase, beta 1 /DB_XREF=gi:10834965 /UG=Hs.79222 galactosidase, beta 1 /FL=gb:NM 000404.1 gb:M27507.1 gb:NM2590.1 qb:NM34423.1
202548_s_at	gb:NM_003899.1 /DEF=Homo sapiens PAK-interacting exchange factor beta /DB_XREF=gi:4505572 /UG=Hs.172813 PAK-interacting exchange factor beta /FL=gb:D63476.1 qb:NM 003699.1
204028_s_at	gb:NM_012197.2 /DEF=Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA. /FEA=mRNA /GEN=GAPCENA /PROD=rab6 GTPase activating protein (GAP and centrosome-associated) /FI=gb:NM 012197.2 qb:XREF=gi:12232372 /UG=Hs.55099 rab6 GTPase activating protein (GAP and centrosome-associated) /FI=gb:NM 012197.2 qb:XREF=est:AU154504 /DB_XREF=gi:11016025 /DB_XREF=est:AU154504 /CLONE=NTWRP4001328
202435_s_at	Consensus includes gb:AU154504 /FEA=EST /DB_XREF=gi:11016025 /DB_XREF=est:AU154504 /CLONE=NTWRP4001328 /UG=Hs.154654 cytochrome P450, subfamily 1 (diroxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) /FL=gb:NM 000104.2 qb:U03688.1
217980_s_at	gb:NM_017840.1 /DEF=Homo sapiens hypothetical protein FLJ20484 /DB_XREF=gi:8923447 /UG=Hs.5080 hypothetical protein FLJ20484 /PROD=hypothetical protein FLJ20484 /DB_XREF=gi:AF275806.1 qb:BC001040.1 qb:NM 017840.1 qb:AF183420.1
201112_s_at	gb:NM_001316.1 /DEF=Homo sapiens chromosome 1 (yeast homolog)-like (CSE1L), mRNA. /FEA=mRNA /GEN=CSE1L /PROD=chromosome segregation 1 (yeast homolog)-like /DB_XREF=gi:4503072 /UG=Hs.90073 chromosome segregation 1 (yeast homolog)-like /FL=gb:U33286.1 qb:AF053341.1 qb:NM 001316.1
202322_s_at	gb:NM_004837.1 /DEF=Homo sapiens geranylgeranyl diphosphate synthase 1 (GGPS1), mRNA. /FEA=mRNA /GEN=GGPS1 /PROD=geranylgeranyl diphosphate synthase 1 /DB_XREF=gi:4758429 /UG=Hs.55498 geranylgeranyl diphosphate synthase 1 /FL=gb:AF051698.1 qb:BC005252.1 qb:AB016043.1 qb:AB019036.1 qb:NM 004837.1 qb:AF125394.1
203545_at	gb:NM_024019.1 /DEF=Homo sapiens hypothetical protein MGC2840 similar to a putative glucosyltransferase (MGC2840), mRNA. /FEA=mRNA /GEN=MGC2840 /PROD=hypothetical protein MGC2840 similar to a putative glucosyltransferase /DB_XREF=gi:13129069 /UG=Hs.155556 hypothetical protein MGC2840 similar to a putative glucosyltransferase /FL=gb:BC001133.1 qb:NM 024019.1
212646_at	Consensus includes gb:D42043.1 /DEF=Human mRNA for KIAA0084 gene, partial cds. /FEA=mRNA /GEN=KIAA0084 /DB_XREF=gi:577298 /UG=Hs.79123 KIAA0084 protein
212591_at	Consensus includes gb:AA887480 /FEA=EST /DB_XREF=gi:3003168 /DB_XREF=est:oj54a12.s1 /CLONE=IMAGE:15021110 /UG=Hs.17428 RBP1-like protein
218005_at	Consensus includes gb:AA744771 /FEA=EST /DB_XREF=gi:2783535 /DB_XREF=est:ny7id07.s1 /CLONE=IMAGE:1283725 /UG=Hs.108482 zinc finger protein 22 (KOX 15) /FL=gb:NM 006963.1
201165_s_at	Consensus includes gb:BB670915 /FEA=EST /DB_XREF=est:7ed3a09.x1 /CLONE=IMAGE:32855208 /UG=Hs.153334 pumilio (Drosophila) homolog I /FL=gb:AF355592.1 qb:NM 014676.1
212239_at	Consensus includes gb:AI680192 /FEA=EST /DB_XREF=gi:4890374 /DB_XREF=est:tw66a10.x1 /CLONE=IMAGE:2264634 /UG=Hs.6241 phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
204386_s_at	Consensus includes gb:BF303597 /FEA=EST /DB_XREF=gi:11250218 /DB_XREF=est:60188623012 /CLONE=IMAGE:4120146 /UG=Hs.182695 hypothetical protein MGC3243 /FL=gb:BC000002.1 qb:NM 024026.1
214853_s_at	Consensus includes gb:AI091079 /FEA=EST /DB_XREF=gi:3430138 /DB_XREF=est:qa33e05.s1 /CLONE=IMAGE:1690496 /UG=Hs.81912 SHC (Src homology 2 domain-containing) transforming protein 1
210580_x_at	gb:125275.1 /DEF=human estrogen sulfotransferase mRNA, complete cds. /FEA=mRNA /PROD=estrogen sulfotransferase /DB_XREF=gi:463124 /UG=Hs.274614 sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /FL=gb:L25275.1
222150_s_at	Consensus includes gb:AK026747.1 /DEF=Homo sapiens cDNA: FLJ23094 fis, clone ING07379, highly similar to HST000007 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 293605. /FEA=mRNA /DB_XREF=gi:10439670 /UG=Hs.12969 hypothetical protein /DB_XREF=gi:BC001650.1 /DEF=Homo sapiens, Similar to putative methyltransferase, Clone MGC.2708, mRNA, complete cds. /FEA=mRNA /PROD=Similar to putative methyltransferase /DB_XREF=gi:12804482 /UG=Hs.268149 putative methyltransferase /FL=gb:BC003031.1 qb:BC001650.1 qb:NM 019852.1
209265_s_at	

218807_at	gb:NM_006113.2 /DEF=Homo sapiens vav 3 oncogene (VAV3), mRNA. /FEA=mRNA /GEN=VAV3 /PROD=vav 3 oncogene /DB_XREF=gi:7262390
209043_at	gb:AF033026.1 /DEF=Homo sapiens bifunctional ATP sulfurylaseadenosine 5'-phosphosulfate kinase mRNA, complete cds. /FEA=mRNA /PROD=bifunctional ATP sulfurylaseadenosine 5'-phosphosulfate kinase /FL=gi:3378100
219777_at	gb:NM_024711.1 /DEF=Homo sapiens hypothetical protein FLJ2290 (FLJ22690), mRNA. /FEA=mRNA /GEN=FLJ22690 /PROD=hypothetical protein FLJ2290 /DB_XREF=gi:13376008 /UG=hs_105468 hypothetical protein FLJ22690 /FL=gb:NM_024711.1
218048_at	gb:NM_012071.1 /DEF=Homo sapiens BUP protein (BUP), mRNA. /FEA=mRNA /GEN=BUP /PROD=BUP protein /DB_XREF=gi:6912277 /UG=hs_35660 BUP protein /FL=gb:AF078848.1 gb:AF201948.1 gb:NM_012071.1
201986_at	Consensus includes gb:AB011165.1 /DEF=Homo sapiens mRNA for KIAA0593 protein, partial cds. /FEA=mRNA /GEN=KIAA0593 /PROD=KIAA0593 protein /DB_XREF=gi:3043709 /UG=hs_11861 thyroid hormone receptor-associated protein, 240 kDa subunit /FL=gb:AF117754.1 gb:NM_005121.1
219799_s_at	gb:NM_005771.1 /DEF=Homo sapiens retinol dehydrogenase homolog (RDHL), mRNA. /FEA=mRNA /GEN=RDHL /PROD=retinol dehydrogenase homolog /DB_XREF=gi:5032034 /UG=hs_179608 retinol dehydrogenase homolog /FL=gb:AF067174.1 gb:NM_005771.1
208888_x_at	gb:UT8525.1 /DEF=Homo sapiens eukaryotic translation initiation factor (eIF3) mRNA, complete cds. /FEA=mRNA /GEN=eIF3 /PROD=eukaryotic translation initiation factor /DB_XREF=gi:2558667 /UG=hs_57783 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) /FL=gb:U78525.1
200001_at	gb:NM_001749.1 /DEF=Homo sapiens calpain 4, small subunit (30k) (CAPN4), mRNA. /FEA=mRNA /GEN=CAPN4 /PROD=calpain 4 small subunit /DB_XREF=gi:4502564 /UG=hs_74451 calpain 4, small subunit (30k) /FL=gb:BC000592.1 gb:NM_001749.1
218118_s_at	gb:NM_006327.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 23 (yeast) homolog (TIM23), mRNA. /GEN=TIM23 /PROD=translocase of inner mitochondrial membrane 23 (yeast) homolog /DB_XREF=gi:554121 /UG=hs_28364 translocase of inner mitochondrial membrane 23 (yeast) homolog /FL=gb:AF030162.1 gb:NM_006327.1
201840_at	gb:NM_006156.1 /DEF=Homo sapiens neural precursor cell expressed, developmentally down-regulated 8 (NEDD8), mRNA. /FEA=mRNA /GEN=NEDD8 /PROD=neural precursor cell expressed, developmentally down-regulated 8 (NEDD8), mRNA. /UG=hs_75512 neural precursor cell expressed, developmentally down-regulated 8 /FL=gb:D23662.1 gb:NM_006156.1
38710_at	Cluster Incl. AL096714:Homo sapiens mRNA; cDNA DKF2p564E242 (From clone DKF2p564E242) /cds=UNKNOWN /gb=AL096714 /gi=3419847 /ug=hs_108504 /len=1904
212287_at	Consensus includes gb:BP382924 /FEA=EST /DB_XREF=gi:11364313 /DB_XREF=est:601816985FL /CLONE=IMAGE:4050909 /UG=hs_197803 KIAA0160 protein
203098_at	Consensus includes gb:AL050164.1 /DEF=Homo sapiens mRNA; cDNA DKF2p586C1622 (from clone DKF2p586C1622); partial cds. /FEA=mRNA /GEN=DKF2p586C1622 /PROD=hypothetical protein /DB_XREF=gi:4884378 /UG=hs_16081 chromodomain protein, y chromosome-like /FL=gb:AF081258.1 gb:AF081259.1 gb:NM_004824.1
218905_at	gb:NM_017864.1 /DEF=Homo sapiens hypothetical protein FLJ20530 (FLJ20530), mRNA. /FEA=mRNA /GEN=FLJ20530 /PROD=hypothetical protein FLJ20530 /DB_XREF=gi:8923495 /UG=hs_279521 hypothetical protein FLJ20530 /FL=gb:NM_017864.1
218303_x_at	gb:NM_016618.1 /DEF=Homo sapiens hypothetical protein (LOC51315), mRNA. /FEA=mRNA /GEN=LOC51315 /PROD=hypothetical protein /DB_XREF=gi:7706155 /UG=hs_5721 hypothetical protein /FL=gi:13414251 /DB_XREF=est:602326894FL /CLONE=IMAGE:4650406
208705_s_at	Consensus includes gb:BG481972 /FEA=EST /DB_XREF=gi:13414251 /DB_XREF=est:602326894FL /CLONE=IMAGE:4650406 /UG=hs_286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1
218715_at	gb:NM_018428.1 /DEF=Homo sapiens hepatocellular carcinoma-associated antigen 66 (HCA66), mRNA. /FEA=mRNA /GEN=HCA66 /PROD=hepatocellular carcinoma-associated antigen 66 /DB_XREF=gi:8923721 /UG=hs_30670 hepatocellular carcinoma-associated antigen 66 /FL=gb:AF244135.1 gb:NM_018428.1
202184_s_at	gb:NM_018230.1 /DEF=Homo sapiens hypothetical protein FLJ10814 (FLJ10814), mRNA. /FEA=mRNA /GEN=FLJ10814

202004_x_at	/PROD=hypothetical protein FLJ10814 /DB_XREF=gi:8922689 /UG=Hs.12457 hypothetical protein FLJ10814 /FI=gb:NM_018230.1 gb:NM_003001.2 /DEF=Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kd (SDHC), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=SDHC /PROD=succinate dehydrogenase complex, subunit C precursor /DB_XREF=gi:9257243 /UG=Hs.3577 succinate dehydrogenase complex, subunit C, integral membrane protein, 15kd /FI=gb:U57877.1 qb:NM_003001.2
209435_s_at	gb:BC00265.1 /DEF=Homo sapiens, clone MGC:3182, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:3182) /DB_XREF=gi:12653008 /UG=Hs.315417 Homo sapiens, clone MGC:3182, mRNA, complete cds. /FI=gb:BC00265.1
221044_s_at	gb:NM_021616.1 /DEF=Homo sapiens ring finger protein 21, interferon-responsive /DB_XREF=gi:11055977 /UG=Hs.125300 ring finger protein 21, interferon-responsive /FL=gb:AB035903.1 qb:NM_021616.1
200932_at	Consensus includes gb:AL137335.1 /DEF=Homo sapiens mRNA; cDNA DKF2p434A179 (from clone DKF2p434A179); partial cds. /FEA=mRNA /GEN=DKF2p434A179 /PROD=hypothetical protein /FL=gb:AE098799.1 qb:NM_006391.1 /FL=gb:AE098799.1 qb:NM_006391.1
201900_s_at	gb:NM_006066.1 /DEF=Homo sapiens aldo-keto reductase family 1, member A1 (aldehyde reductase) (AKR1A1), mRNA. /FEA=mRNA /GEN=AKR1A1 /PROD=aldo-keto reductase family 1, member A1 (aldehyde reductase) /DB_XREF=gi:5174390 /UG=Hs.89529 aldo-keto reductase family 1, member A1 (aldehyde reductase) /FI=gb:BC000670.1 qb:J04794.1 qb:NM_006066.1
202560_s_at	gb:NM_015607.1 /DEF=Homo sapiens DKFZP547E1010 protein (DKFZP547E1010), mRNA. /GEN=DKFZP547E1010 /PROD=DKFZP547E1010 protein /DB_XREF=gi:7661589 /UG=Hs.323817 DKFZP547E1010 protein /FI=gb:NM_015607.1
201105_at	gb:NM_0022305.2 /DEF=Homo sapiens lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA. /FEA=mRNA /GEN=LGALS1 /PROD=beta-galactosidase binding lectin precursor /DB_XREF=gi:6006015 /UG=Hs.227751 lectin, galactoside-binding, soluble, 1 (galectin 1) /FI=gb:BC001953.1 qb:J04456.1 qb:NM_0022305.2
204546_at	gb:NM_014732.1 /DEF=Homo sapiens KIAA0513 gene product (KIAA0513), mRNA. /FEA=mRNA /GEN=KIAA0513 /PROD=KIAA0513 gene product /DB_XREF=gi:7662163 /UG=Hs.301658 KIAA0513 gene product /FI=gb:AB011085.1 qb:NM_014732.1
211181_x_at	Consensus includes gb:AT735692 /FEA=EST /DB_XREF=gi:5057216 /DB_XREF=est:at20512.x1 /CLONE=IMAGE:2355647 /UG=Hs.88411 lymphocyte antigen 117
219032_x_at	gb:NM_014322.1 /DEF=Homo sapiens opsin 3 (encephalopsin) (OPN3), mRNA. /FEA=mRNA /GEN=OPN3 /PROD=opsin 3 (encephalopsin) /DB_XREF=gi:7657070 /UG=Hs.279926 opsin 3 (encephalopsin) /FI=gb:AF140242.1 qb:NM_014322.1
205306_x_at	Consensus includes gb:AI074145 /FEA=EST /DB_XREF=gi:340789 /DB_XREF=est:afv13a06.x1 /CLONE=IMAGE:1637170 /UG=Hs.107318 kynurenone 3-monooxygenase (kynurenone 3-hydroxylase) /FI=gb:AF056032.1 qb:NM_03679.1
202837_at	gb:NM_006700.1 /DEF=Homo sapiens FLN29 gene product (FLN29), mRNA. /FEA=mRNA /GEN=FLN29 /PROD=FLN29 gene product /DB_XREF=gi:5729827 /UG=Hs.5148 FLN29 gene product /FI=gb:BC003555.1 qb:AB007447.1 qb:NM_006700.1
202153_s_at	gb:NM_016553.1 /DEF=Homo sapiens hypothetical protein (DKFZP547L134), mRNA. /FEA=mRNA /GEN=DKFZP547L134 /PROD=hypothetical protein /DB_XREF=gi:70705354 /UG=Hs.9877 hypothetical protein /FI=gb:AL162061.1 qb:NM_016553.1
209341_s_at	Consensus includes gb:AU153366 /FEA=EST /DB_XREF=gi:11014887 /DB_XREF=est:AU153366 /CLONE=NT2RP3002988 /UG=Hs.226573 inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta /FI=gb:AF031416.1 qb:AF080158.1
212493_s_at	Consensus includes gb:AI761110 /FEA=EST /DB_XREF=gi:5176777 /DB_XREF=est:w169n02.x1 /CLONE=IMAGE:2398611 /UG=Hs.6947 HSPO69 protein
201600_at	gb:NM_007273.1 /DEF=Homo sapiens B-cell associated protein (REA), mRNA. /FEA=mRNA /GEN=REA /PROD=B-cell associated protein /FI=gb:AF126021.1 gb:AF178780.1
201144_s_at	gb:NM_004094.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kd) (EIF2S1), mRNA. /FEA=mRNA /GEN=EIF2S1 /PROD=eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kd) /DB_XREF=gi:475255 /UG=Hs.151777 eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kd) /FI=gb:BC002513.1 qb:J02645.1
211985_s_at	Consensus includes gb:AI653730 /FEA=EST /DB_XREF=gi:4737709 /DB_XREF=est:wb36f12.x1 /CLONE=IMAGE:2307791 /UG=Hs.279009 matrix Gla protein

201226_at	gb:NM_005004.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI) (NDUFB8), mRNA. /FEA=mRNA /GEN=NDUFB8 /PROB=NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 8 (19kD, ASHI) /DB_XREF=gi:4826853 /UG=Hs_198273 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI) /FL=gb:BC004466.1 gb:AF044058.1 gb:AF07028.1 gb:NM_005004.1
208828_at	gb:BC004170.1 /DEF=Homo sapiens, histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit, clone MGC:2725, mRNA, complete cds. /FEA=mRNA /PROB=histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit /FL=gb:BC003166.1 gb:BC004170.1 /UG=Hs_108112 histone fold protein CHRAC17; DNA polymerase epsilon p17 subunit /FL=gb:NM_017443.1 gb:AF226077.1 gb:NM_017443.1
204020_at	Consensus includes gb:BF739943 /FEA=EST /DB_XREF=gi:12066607 /DB_XREF=est:7o41b04.x1 /CLONE=IMAGE:3576534 /UG=Hs_29117 purine-rich element binding protein A /FL=gb:NM_096684.1 qb:NM_005859.1
217942_at	gb:NM_021821.1 /DEF=Homo sapiens MDS023 protein (MDS023), mRNA. /FEA=mRNA /GEN=MDS023 /PROD=MDS023 protein /DB_XREF=gi:11141894 /UG=Hs_10724 MDS023 protein /FL=gb:AF182422.1 qb:NM_021821.1
203514_at	Consensus includes gb:BF971923 /FEA=EST /DB_XREF=gi:12339138 /DB_XREF=est:6022403226f1 /CLONE=IMAGE:4328791 /UG=Hs_29282 mitogen-activated protein kinase kinase kinase 3 /FL=gb:U78876.1 qb:NM_002401.1
204334_at	Consensus includes gb:AA488672 /FEA=EST /DB_XREF=gi:2216103 /DB_XREF=est:ab40d10.s1 /CLONE=IMAGE:843283 /UG=Hs_21599 Kruppel-like factor 7 (ubiquiFons) /FL=gb:AB015132.1 qb:NM_003709.1
203531_at	Consensus includes gb:BF435809 /FEA=EST /DB_XREF=gi:11448124 /DB_XREF=est:nab42a09.x1 /CLONE=IMAGE:3268504 /UG=Hs_101299 cullin 5 /FL=gb:AF227710.1 qb:AB017061.1 qb:NM_003478.1
205022_s_at	gb:NM_005197.1 /DEF=Homo sapiens checkpoint suppressor 1 (CHESS1), mRNA. /FEA=mRNA /GEN=CHESS1 /PROD=checkpoint suppressor 1 /DB_XREF=gi:4885136 /UG=Hs_211773 checkpoint suppressor 1 /FL=gb:U68723.1 qb:NM_005197.1
201532_at	gb:NM_002788.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3), mRNA. /FEA=mRNA /GEN=PSMA3 /PROD=proteasome (prosome, macropain) subunit, alphatype, 3 /DB_XREF=gi:4506182 /UG=Hs_167106 proteasome (prosome, macropain) subunit, alpha type, 3 /FL=gb:BC005265.1 qb:NM_002788.1
204972_at	gb:NM_016817.1 /DEF=Homo sapiens 2'-S oligoadenylylate synthetase 2 (OAS2), transcript variant 1, mRNA. /FEA=mRNA /GEN=OAS2 /PROD=2'-S oligoadenylylate synthetase 2, isoform p71 /DB_XREF=gi:8051624 /UG=Hs_261981 2'-S oligoadenylylate synthetase 2 /FL=gb:MR7434.1 qb:NM_016817.1
209200_at	Consensus includes gb:AL536517 /FEA=EST /DB_XREF=gi:12800010 /DB_XREF=est:AL536517 /CLONE=CSDF0387YH13 (5 prime) /UG=Hs_78995 MADS box transcription enhancer factor 2C /FL=gb:108895.1
217945_at	gb:NM_025238.1 /DEF=Homo sapiens BTB (POZ) domain containing 1 (BTBD1), mRNA. /FEA=mRNA /GEN=BTBD1 /PROD=BTBD1 (POZ) domain containing 1 /DB_XREF=gi:13376347 /UG=Hs_21332 BTB (POZ) domain containing 1 /FL=gb:AB1136853.1 gb:AB257241.1 qb:NM_0255738.1 qb:AF355402.1
201491_at	gb:NM_012111.1 /DEF=Homo sapiens chromosome 14 open reading frame 3 (C14orf3), mRNA. /FEA=mRNA /GEN=C14orf3 /PROD=chromosome 14 open reading frame 3 /DB_XREF=gi:6912219 /UG=Hs_204041 chromosome 14 open reading frame 3 /FL=gb:BC00321.1 qb:NM_012111.1 qb:AF164791.1
204868_at	gb:NM_001545.1 /DEF=Homo sapiens immature colon carcinoma transcript 1 /DB_XREF=gi:4557656 /UG=Hs_9078 immature colon carcinoma transcript 1 /FL=gb:NM_001545.1
217826_s_at	gb:NM_016021.1 /DEF=Homo sapiens CGI-76 protein (LOC51632), mRNA. /FEA=mRNA /GEN=LOC51632 /PROD=CGI-76 protein /DB_XREF=gi:7706311 /UG=Hs_184325 CGI-76 protein /FL=gb:AF51834.1 qb:AF151039.1 qb:NM_016021.1
212534_at	Consensus includes gb:AU144066 /FEA=EST /DB_XREF=gi:111005567 /DB_XREF=est:AU144066 /CLONE=HEMBA1000798 /UG=Hs_285519 Homo sapiens CDNA FLJ11904 fis, Clone HEMBB100048
211284_s_at	gb:BC000324.1 /DEF=Homo sapiens, similar to granulin, clone MGC:6480, mRNA, complete cds. /FEA=mRNA /PROD=Similar to granulin /DB_XREF=gi:12653114 /UG=Hs_180577 granulin /FL=gb:BC000324.1
212188_at	Consensus includes gb:AA51075 /FEA=EST /DB_XREF=gi:2321327 /DB_XREF=est:nk74h06.s1 /CLONE=IMAGE:1019291 /UG=Hs_109438 Homo sapiens clone 24775 mRNA sequence

201458_s_at	gb:NM_004725.1 /DEF=Homo sapiens BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog (BUB3), mRNA. /FEA=mRNA /GEN=BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog /FL=gi:4757879 /UG=Hs.40323 BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog /FL=gb:BC005138.1 gb:AF047472.1 qb:AF081496.1 qb:NM_004725.1
201773_at	gb:NM_015339.1 /DEF=Homo sapiens activity-dependent neuroprotective protein (ADNP), mRNA. /FEA=mRNA /GEN=ADNP /PROD=activity-dependent neuroprotective protein /DB_XREF=gi:12229216 /UG=Hs.3657 activity-dependent neuroprotective protein /FL=qb:AF250860.1 qb:NM_015339.1
218751_s_at	gb:NM_018315.1 /DEF=Homo sapiens hypothetical protein FLJ11071 (FLJ11071), mRNA. /FEA=mRNA /GEN=FLJ11071 /PROD=hypothetical protein FLJ11071 /DB_XREF=gi:8922851 /UG=Hs.31945 hypothetical protein FLJ11071 /FL=gb:NM_018315.1 /UG=Is.184488 flotillin 2 FL=qb:NM_004475.1 qb:M60922.1
201350_at	gb:NM_004475.1 /DEF=Homo sapiens flotillin 2 (FLOT2), mRNA. /FEA=mRNA /GEN=FLOT2 /PROD=flotillin 2 /DB_XREF=gi:4758393 /UG=Is.184488 flotillin 2 FL=qb:NM_004475.1 qb:M60922.1
201098_at	gb:NM_004766.1 /DEF=Homo sapiens coatomer protein complex, subunit beta 2 (beta prime) (COPB2), mRNA. /FEA=mRNA /GEN=COPB2 /PROD-coatomer protein complex, subunit beta 2 (beta prime) /FL=qb:BC000326.1 qb:NM_004766.1
203732_at	gb:NM_016213.1 /DEF=Homo sapiens thyroid hormone receptor interactor 4 (TRIP4), mRNA. /FEA=mRNA /GEN=TRIP4 /PROD-activating signal cointegrator 1 /DB_XREF=gi:7706430 /UG=Hs.116784 thyroid hormone receptor interactor 4 /FL=qb:AF168418.1 qb:NM_016213.1
202846_s_at	gb:NM_002642.1 /DEF=Homo sapiens phosphatidylinositol glycan, class C (PIGC), mRNA. /FEA=mRNA /GEN=PIGC /PROD-Phosphatidylinositol glycan, class C /DB_XREF=gi:4505794 /UG=Hs.75790 phosphatidylinositol glycan, class C /FL=qb:D85418.1 qb:NM_002642.1
205936_s_at	gb:NM_002115.1 /DEF=Homo sapiens hexokinase 3 (white cell) (HK3), mRNA. /FEA=mRNA /GEN=HK3 /PROD=hexokinase 3 (white cell) /DB_XREF=gi:1504394 /UG=Hs.159237 hexokinase 3 (white cell) /FL=qb:U51333.1 qb:NM_002115.1
201209_at	gb:NM_004964.2 /DEF=Homo sapiens histone deacetylase 1 (HDAC1), mRNA. /FEA=mRNA /GEN=HDAC1 /PROD=histone deacetylase 1 /DB_XREF=gi:13128859 /UG=Hs.885556 histone deacetylase 1 /FL=qb:BC000301.1 qb:NM_004964.2 qb:D50405.1
217798_at	Consensus includes gb:AI123426 /FEA=EST /DB_XREF=gi:3539192 /DB_XREF=est:q49c09.x1 /CLONE=IMAGE:1690096 /UG=Is.239720 CCR4-NOT transcription complex, subunit 2 /FL=qb:AF113226.1 qb:AF180473.1 qb:NM_014515.1
209455_at	Consensus includes gb:BE963245 /FEA=EST /DB_XREF=gi:11766663 /DB_XREF=est:601656874R1 /CLONE=IMAGE:3865699 /UG=Hs.21229 f-box and WD-40 domain protein 1B /FL=qb:AF176022.1 qb:AB033281.1
212397_at	Consensus includes gb:AI137751.1 /DEF=Homo sapiens mRNA; cDNA DKF2p434I0812 (From clone DKF2p434I0812); partial cds. /FEA=mRNA /GEN=DKF2p434I0812 (from clone DKF2p434I0812); partial cds
218025_s_at	gb:NM_006117.1 /DEF=Homo sapiens peroxisomal D3, D2-enoyl-CoA isomerase (PECI), mRNA. /FEA=mRNA /GEN=PECI /PROD-peroxisomal D3, D2-enoyl-CoA isomerase /DB_XREF=gi:5174624 /UG=Hs.15250 peroxisomal D3, D2-enoyl-CoA isomerase /FL=qb:AI136642.1 qb:BC02668.1 qb:AF069301.1 qb:AF153612.1 qb:NM_006117.1 qb:AF244138.1
203217_s_at	gb:NM_003896.1 /DEF=Homo sapiens sialyltransferase 9 (CMP-Neuac: lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (ST9), mRNA. /FEA=mRNA /GEN=ST9 /PROD=sialyltransferase 9 (CMP-Neuac: lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) /DB_XREF=gi:4506954 /UG=Hs.225939 sialyltransferase 9 (CMP-Neuac: lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) /FL=qb:AB018356.1 qb:NM_003896.1 qb:AF119415.1
212812_at	Consensus includes gb:AI1700633 /FEA=EST /DB_XREF=gi:4988533 /DB_XREF=est:we38903.x1 /CLONE=IMAGE:2343412 /UG=Hs.288232 Homo sapiens cDNA: FLJ22642 f.s., clone HSI06970
207830_s_at	gb:NM_002713.1 /DEF=Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 8 (PPP1R8), mRNA. /GEN=PPP1R8 /PROD-protein phosphatase 1, regulatory (inhibitor) subunit 8 /DB_XREF=gi:4506014 /UG=Hs.78961 protein phosphatase 1, regulatory (inhibitor) subunit 8 /FL=qb:NM_002713.1 qb:U14575.1
204061_at	gb:NM_005044.1 /DEF=Homo sapiens protein kinase, X-linked (PRKX), mRNA. /FEA=mRNA /GEN=PRKX /PROD=protein kinase, X-linked /DB_XREF=gi:4826547 /UG=Hs.147996 protein kinase, X-linked /FL=qb:NM_005044.1

215633_x_at	Consensus includes gb:AV713720 / FEA=EST /DB_XREF=gi:10795237 /DB_XREF=est:AV713720 /CLONE=DCBBA12 /UG=Hs .306434 Homo sapiens mRNA for LST-1N protein
208660_at	gb:BC000105.1 /DEF=Homo sapiens, Similar to CG14740 gene product /DB_XREF=gi:12652712 /UG=Hs .239760 citrate synthase /FI=gb:BC000105.1 gb:AF047042.1 /PROD=Similar to CG14740 gene product
218805_at	gb:NM_018384.1 /DEF=Homo sapiens hypothetical protein FLJ11296 /DB_XREF=gi:89229984 /UG=Hs .26194 hypothetical protein FLJ11296 /FI=gb:NM_018384.1 /PROD=hypothetical protein
217725_x_at	gb:NM_015640.1 /DEF=Homo sapiens PAI-1 mRNA-binding protein (PAI-RBP1), mRNA. /FEA=mRNA /GEN=PAI-RBP1 /PROD=PAI-1 mRNA-binding protein /DB_XREF=gi:7661625 /UG=Hs .165998 PAI-1 mRNA-binding protein /FI=gb:AU080119.1 gb:NM_015640.1
200802_at	gb:NM_006513.1 /DEF=Homo sapiens seryl-tRNA synthetase (SARS), mRNA. /FEA=mRNA /PROD=seryl-tRNA synthetase /DB_XREF=gi:5730028 /UG=Hs .4888 seryl-tRNA synthetase /FI=gb:BC000716.1 gb:NM_006513.1 gb:D49914.1
213203_at	Consensus includes gb:AI633709 / FEA=EST /DB_XREF=gi:4685039 /DB_XREF=est:th71f03.x1 /CLONE=IMAGE:2124125 /UG=Hs .30174 small nuclear RNA activating complex, polypeptide 5, 19kD
204640_s_at	gb:NM_003563.1 /DEF=Homo sapiens speckle-type POZ protein (SPOP), mRNA. /FEA=mRNA /GEN=SPOP /PROD=speckle-type POZ protein /DB_XREF=gi:4507182 /UG=Hs .129951 speckle-type POZ protein /FI=gb:BC003385.1 gb:NM_003563.1
202324_s_at	gb:NM_022735.1 /DEF=Homo sapiens golgi resident protein GCP60 (GCP60), mRNA. /FEA=mRNA /GEN=GCP60 /PROD=golgi resident protein GCP60 /DB_XREF=gi:12232380 /UG=Hs .6831 golgi resident protein GCP60 /FI=gb:AB043587.1 gb:NM_022735.1
211661_x_at	gb:NM0436.1 /DEF=Human platelet activating factor receptor mRNA, complete cds. /FEA=mRNA /GEN=PTAFR /PROD=Platelet activating factor receptor /DB_XREF=gi:189537 /FI=gb:M80436.1
208969_at	gb:AF050641.1 /DEF=Homo sapiens NADH-ubiquinone oxidoreductase 39kDa subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds. /FEA=mRNA /PROD=NADH-ubiquinone oxidoreductase 39kDa subunit /DB_XREF=gi:5326822 /UG=Hs .75227 (39kD) /FI=gb:AF050641.1 gb:NM_005002.1
202227_s_at	gb:NM_006696.1 /DEF=Homo sapiens thyroid hormone receptor coactivating protein (SMAP), mRNA. /FEA=mRNA /GEN=SMAP /PROD=thyroid hormone receptor coactivating protein /DB_XREF=gi:5730052 /UG=Hs .5464 thyroid hormone receptor coactivating protein /FI=gb:AF016270.1 gb:NM_006696.1
221989_at	Consensus includes gb:AW057781 / FEA=EST /DB_XREF=gi:5933420 /DB_XREF=est:wx03f09.x1 /CLONE=IMAGE:2542601 /UG=Hs .29797 ribosomal protein L10
202545_at	gb:NM_006254.1 /DEF=Homo sapiens protein kinase C, delta (PRKCD), mRNA. /FEA=mRNA /GEN=PRKCD /PROD=protein kinase C, delta /DB_XREF=gi:515453969 /UG=Hs .155342 protein kinase C, delta /FI=gb:AB014595.1
202214_s_at	gb:NM_003588.1 /DEF=Homo sapiens cullin 4B (CUL4B), mRNA. /FEA=mRNA /GEN=CUL4B /PROD=cullin 4B /DB_XREF=gi:13270466 /UG=Hs .155976 cullin 4B /FI=gb:NM_003588.1 gb:AB014595.1
218366_x_at	gb:NM_022734.1 /DEF=Homo sapiens hypothetical protein FLJ20859 (FLJ20859), mRNA. /FEA=mRNA /GEN=FLJ20859 /PROD=hypothetical protein FLJ20859 /DB_XREF=gi:12232388 /UG=Hs .6311 hypothetical protein FLJ20859 /FI=gb:NM_022734.1
218592_s_at	gb:NM_017829.1 /DEF=Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA. /FEA=mRNA /GEN=FLJ20454 /PROD=hypothetical protein FLJ20454 /DB_XREF=gi:8923424 /UG=Hs .26890 hypothetical protein FLJ20454 /FI=gb:AF273271.1
209658_at	gb:AF164598.1 /DEF=Homo sapiens cell division control protein 16 (CDC16) mRNA, complete cds. /FEA=mRNA /GEN=CDC16 /PROD=cell division control protein 16 /DB_XREF=gi:5533374 /UG=Hs .1592 CDC16 (cell division cycle 16, S. cerevisiae, homolog) /FI=gb:AF164598.1
202217_at	gb:NM_004649.1 /DEF=Homo sapiens ESI (zebrafish) protein, human homolog of (C21ORF33), mRNA. /FEA=mRNA /GEN=C21ORF33 /PROD=ESI (zebrafish) protein, human homolog of /DB_XREF=gi:503190 /UG=Hs .182423 ESI (zebrafish) protein, human homolog of /FI=gb:BC002370.1 gb:BC003387.1 gb:D86061.1 gb:U53003.1 gb:NM_004649.1
54970_at	Cluster Incl. AA868332:ak40h05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1408173 /clone_end=3 /gb=AA868332 /gi=2963777 /ug=Hs .77978 /len=481

202441_at	Consensus includes gb:AL568449 /FEA=EST /DB_XREF=gi:12922799 /DB_XREF=est:AL568449 /CLONE=CSODE001YC12 (3 prime) /UG=Hs.285818 similar to <i>Caenorhabditis elegans</i> protein C42C1.9 /FL=gb:AY064093.1 qb:NM 006459.1
211383_s_at	gb:AL136827.1 /DEF=Homo sapiens mRNA; cDNA DK2Zp434F2427 (from clone DK2Zp434F2427); complete cds. /FEA=mRNA /GEN=DKFZp434F2427 /PROD=hypothetical protein /DB_XREF=gi:6807664 /UG=Hs.27207 KIAA0982 protein /FL=gb:AL136827.1
201903_at	gb:NM_003365.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase core protein I (UQCRC1), mRNA. /FEA=mRNA /GEN=UQCRC1 /PROD=ubiquinol-cytochrome C reductase core protein I /DB_XREF=gi:4507840 /UG=Hs.119251 ubiquinol-cytochrome C reductase core protein I /FL=gb:U116842.1 qb:NM 003365.1 qb:D26485.1
201827_at	gb:AF113019.1 /DEF=Homo sapiens PRO2451 mRNA, complete cds. /FEA=mRNA /PROD=PRO2451 /DB_XREF=gi:6642761 /UG=Hs.250581 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 /FL=gb:U66618.1 qb:NM 003071.1 qb:AF113019.1
201583_s_at	gb:NM_006363.1 /DEF=Homo sapiens Sec23 (S. cerevisiae) homolog B (SEC23B), mRNA. /FEA=mRNA /GEN=SEC23B /PROD=Sec23 (S. cerevisiae) homolog B /DB_XREF=gi:5454043 /UG=Hs.173497 Sec23 (S. cerevisiae) homolog B /FL=gb:BC005404.1 qb:NM 006363.1 gb:AF130103.1 /DEF=Homo sapiens clone FIB2914 PRO0720 mRNA, complete cds. /FEA=mRNA /PROD=PRO0720 /DB_XREF=gi:11493509 /UG=Hs.1160483 erythrocyte membrane protein band 7.2 (stomatin) /FL=gb:AF130103.1
212696_s_at	Consensus includes gb:BF958633 /FEA=EST /DB_XREF=gi:12335848 /DB_XREF=est:602271068F1 /CLONE=IMAGE:4359209 /UG=Hs.66394 ring finger protein 4
218229_s_at	gb:NM_017542.1 /DEF=Homo sapiens KIAA1513 protein (KIAA1513), mRNA. /FEA=mRNA /GEN=KIAA1513 /PROD=KIAA1513 protein /DB_XREF=gi:8923835 /UG=Hs.284227 KIAA1513 protein /FL=gb:NM 017542.1
210111_s_at	gb:AF277175.1 /DEF=Homo sapiens PNAS-138 mRNA, complete cds. /FEA=mRNA /PROD=PNAS-138 /DB_XREF=gi:12751080 /UG=Hs.326790 Homo sapiens PNAS-138 mRNA, complete cds /FL=gb:AF277175.1
201268_at	gb:NM_002512.1 /DEF=Homo sapiens non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=NME2 /PROD=non-metastatic cells 2, protein (NM23B), protein (NM23B) expressed in /DB_XREF=gi:4505408 /UG=Hs.275163 non-metastatic cells 2, protein (NM23B) expressed in /FL=gb:BC002476.1 qb:M36981.1 qb:NM 002512.1
201199_s_at	gb:NM_002807.1 /DEF=Homo sapiens proteasome (prosome, macropain) 26S subunit, non-APase, 1 (PSMD1), mRNA. /FEA=mRNA /GEN=PSMD1 /PROD=proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 /DB_XREF=gi:4506224 /UG=Hs.3887 proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 /FL=gb:D44466.1 qb:NM 002807.1
218242_s_at	gb:NM_017635.1 /DEF=Homo sapiens hypothetical protein FLJ20039 (FLJ20039), mRNA. /FEA=mRNA /GEN=FLJ20039 /PROD=hypothetical protein FLJ20039 /DB_XREF=gi:8923045 /UG=Hs.267448 hypothetical protein FLJ20039 /FL=gb:NM 017635.1
201232_s_at	gb:NM_002817.1 /DEF=Homo sapiens proteasome (prosome, macropain) 26S subunit, non-APase, 13 (PSMD13), mRNA. /FEA=mRNA /GEN=PSMD13 /PROD=proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 /DB_XREF=gi:4506222 /UG=Hs.279554 proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 /FL=gb:BC001100.1 qb:BC001747.1 qb:AB009398.1
220044_x_at	gb:NM_016424.1 /DEF=Homo sapiens cisplatin resistance-associated overexpressed protein (LUC7A), mRNA. /GEN=LUC7A /PROD=cisplatin resistance-associated overexpressed protein /FL=gb:NM 016424.1 -
210835_s_at	gb:AF222711.1 /DEF=Homo sapiens ribeye mRNA, complete cds. /FEA=mRNA /PROD=ribeye /DB_XREF=gi:12034652 /UG=Hs.171391 cisplatin resistance-associated overexpressed protein 2 /FL=gb:AF222711.1 qb:NM 022802.1
211271_x_at	gb:BC004383.1 /DEF=Homo sapiens C-terminal binding protein 2 /FL=gb:AF222711.1 qb:NM 022802.1 Similar to polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I), clone MCC.1080, mRNA, complete cds. /FEA=mRNA /PROD=similar to polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I) /DB_XREF=gi:1325139 /UG=Hs.172550 polypyrimidine tract binding protein
218998_at	gb:NM_017832.1 /DEF=Homo sapiens hypothetical protein FLJ20457 (FLJ20457), mRNA. /FEA=mRNA /GEN=FLJ20457 /PROD=hypothetical protein FLJ20457 /DB_XREF=gi:8923430 /UG=Hs.29276 hypothetical protein FLJ20457 /FL=gb:AF153417.1 qb:NM 017832.1
201765_s_at	Consensus includes gb:AU523158 /FEA=EST /DB_XREF=gi:12786651 /DB_XREF=est:AU523158 /CLONE=CS0DC001YM06 (3 prime)

204837_at	/UG=Hs.119403 hexosaminidase A (alpha polypeptide) /FL=gb:NM_000520.2
	Consensus includes gb:AL080178.1 /DEF=Homo sapiens mRNA; cDNA DKF2p34K171 (from clone DKF2p34K171); partial cds. /FEA=mRNA /GEN=DKF2p34K171 /PROD=hypothetical protein /DB_XREF=gi:52626552 /UG=Hs.27194 DKF2p34K171 protein /FL=gb:NM_015458.1
201221_s_at	gb:NM_003089.1 /DEF=Homo sapiens small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) (SNRP70), mRNA. /FEA=mRNA /GEN=SNRP70 /PROD=small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen) /EL=gb:BC000342.1 qb:NM_003089.1 polyamide (RNP antigen) /FL=gb:AE151905.1 qb:NM_003089.1
203092_s_at	qb:AB061730.1 /DEF=Homo sapiens clone 016063 Myo27 protein mRNA, complete cds. /FEA=mRNA /PROD=Myo27 protein /DB_XREF=gi:12001995 /UG=Hs.2719061 CG1-150 protein /EL=gb:AF061130.1 qb:AE151905.1 qb:NM_003089.1
202265_at	gb:NM_005180.1 /DEF=Homo sapiens murine leukemia viral (bmi-1) oncogene homolog (BMLF1), mRNA. /FEA=mRNA /GEN=BML1 /PROD=murine leukemia viral_(bmi-1) oncogene homolog /DB_XREF=gi:4885094 /UG=Hs.431 murine leukemia viral (bmi-1) oncogene homolog /FL=gb:J13689.1 qb:NM_005180.1
203721_s_at	qb:NM_016001.1 /DEF=Homo sapiens CGI-48 protein (LOC51096), mRNA. /FEA=mRNA /GEN=LOC51096 /PROD=CGI-48 protein /DB_XREF=gi:7705764 /UG=Hs.6153 CGI-48 protein /FL=gb:AF151806.1 qb:NM_016001.1
202475_at	gb:NM_006326.1 /DEF=Homo sapiens seven transmembrane domain protein (NIFIE4), mRNA. /FEA=mRNA /GEN=NIFIE4 /PROD=seven transmembrane domain protein /DB_XREF=gi:5453781 /UG=Hs.9234 seven transmembrane domain protein /FL=gb:BC001118.1 qb:NM_006326.1
213165_at	Consensus includes gb:AI041204 /FEA=EST /DB_XREF=gi:3280398 /DB_XREF=est:ov7906.x1 /CLONE=IMAGE:1643386 /UG=Hs.323748 Homo sapiens clone CDABP0086 mRNA sequence
213198_at	Consensus includes gb:AI17643.1 /DEF=Homo sapiens mRNA; cDNA DKF2p34M245 (from clone DKF2p34M245). /FEA=mRNA /GEN=KIAA0157 /DB_XREF=gi:915912233 /UG=Hs.5288 Homo sapiens mRNA; cDNA DKF2p34M245 (from clone DKF2p34M245)
212837_at	Consensus includes gb:D63877.1 /DEF=Human mRNA for KIAA0157 gene, partial cds. /FEA=mRNA /GEN=KIAA0157 /DB_XREF=gi:91591445 /UG=Hs.82324
206592_s_at	gb:NM_003938.1 /DEF=Homo sapiens adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA. /FEA=mRNA /GEN=AP3D1 /PROD=adaptor-related protein complex 3, delta 1 subunit /FL=gb:U91930.1 qb:NM_003938.1
212694_s_at	Consensus includes gb:NM_000532.1 /DEF=Homo sapiens propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), nuclear gene encoding mitochondrial protein, mRNA. /FEA=CD5 /GEN=PCCB /PROD=propionyl Coenzyme A carboxylase, betapolypeptide /DB_XREF=gi:4551043 /UG=Hs.63788 propionyl Coenzyme A carboxylase, beta polypeptide /FL=gb:NM_000532.1
211759_x_at	qb:BC005969.1 /DEF=Homo sapiens, clone MG:14625, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:14625) /DB_XREF=gi:13543641 /FL=gb:BC005969.1
212714_at	Consensus includes gb:AL050205.1 /DEF=Homo sapiens mRNA; cDNA DKF2p586F1323 (from clone DKF2p586F1323). /FEA=mRNA /DB_XREF=gi:4384444 /UG=Hs.26613 Homo sapiens mRNA; cDNA DKF2p586F1323
201528_at	Consensus includes gb:BG39414 /FEA=EST /DB_XREF=gi:13291862 /DB_XREF=est:602439888F1 /CLONE=IMAGE:4566380 /UG=Hs.84318 replication protein A1 (70kD) /FL=gb:MG3488.1 qb:NM_002945.1
211795_s_at	qb:AF198052.1 /DEF=Homo sapiens EVH1 domain binding protein RNA, complete cds. /FEA=CDS /PROD=EVH1 domain binding protein /DB_XREF=gi:17416992 /UG=Hs.58435 FYN-binding protein (FYB-120130) /FL=gb:AF198052.1
218633_x_at	qb:NM_018394.1 /DEF=Homo sapiens hypothetical protein FLJ11342, mRNA. /FEA=mRNA /GEN=FLJ11342 /PROD=hypothetical protein FLJ11342 /FL=gb:NM_018394.1
200800_s_at	qb:NM_005315.3 /DEF=Homo sapiens heat shock 70kD protein 1A (HS-P70), mRNA. /FEA=mRNA /GEN=HS-P70A /PROD=heat shock 70kD protein 1A /DB_XREF=gi:5579469 /UG=Hs.8997 heat shock 70kD protein 1A /FL=gb:BC002453.1 qb:NM_005345.3
214719_at	Consensus includes gb:RAK026720.1 /DEF=Homo sapiens cDNA: FLJ72367 fis, clone INGO4993. /FEA=mRNA /DB_XREF=gi:10439638 /UG=Hs.117167 Homo sapiens cDNA: FLJ72367 fis, clone INGO4993
213655_at	Consensus includes gb:AA502643 /FEA=EST /DB_XREF=gi:2237610 /DB_XREF=est:ne42q05.s1 /CLONE=IMAGE:900056 /UG=Hs.79474 tyrosine-3-monooxygenase activation protein, epsilon polypeptide
212371_at	Consensus includes gb:AL093997.1 /DEF=Homo sapiens mRNA; cDNA DKF2p586C1019 (from clone DKF2p586C1019). /FEA=mRNA /DB_XREF=gi:4300188 /UG=Hs.12314
Homo_sapiens_mRNA	cDNA DKF2p586C1019 (from clone DKF2p586C1019)
210166_at	gb:AF051151.1 /DEF=Homo sapiens toll-like receptor-3 (TLL3) mRNA, complete cds. /FEA=mRNA /GEN=TLL3 /PROD=Toll-like receptor-3 /FL=gb:AF051151.1
217959_at	gb:NM_016146.1 /DEF=Homo sapiens PTDD009 protein (PTDD009) /GEN=PTDD009 /PROD=PTDD009 protein /DB_XREF=gi:7706666 /UG=Hs.271901 PTDD009

	/UG-Hs.279901 PTD009 protein /FL=gb:AE15862.1 qb:AE078862.1 qb:AE161520.1 qb:NM_016146.1 gb:NM_021567.1 /DEF=Homo sapiens hypothetical protein FLJ21616 (FLJ21616), mRNA. /FEA=mRNA /GEN=FLJ21616 /PROD=hypothetical protein
219269_at	FLJ21616 /DB_XREF=gi:13375737 /UG-Hs.14562 hypothetical protein FLJ21616 /EL=gb:NM_021567.1
219574_at	gb:NM_017923.1 /DEF=Homo sapiens hypothetical protein FLJ20668 (FLJ20668), mRNA. /FEA=mRNA /GEN=FLJ20668 /PROD=hypothetical protein
210183_x_at	FLJ20668 /DB_XREF=gi:8923612 /UG-Hs.12920 hypothetical protein FLJ20668 /EL=gb:NM_017923.1
210183_x_at	gb:AE112222.1 /DEF=Homo sapiens nuclear protein SDK3 mRNA /PROD=nuclear protein SDK3 /DB_XREF=gi:6563229 /UG-Hs.44499_Pain1 /desmosome associated protein /EL=gb:AE112222.1
211582_x_at	gb:AE000424.1 /DB_XREF=Homo sapiens LST1 mRNA, cLSTIC splice variant, complete cds. /FEA=mRNA /GEN=LST1 /DB_XREF=gi:2145053 /UG-Hs.88411 Lymphocyte antigen 117 /FL=gb:AE000424.1
212557_at	Consensus includes qb:AB011148.1 /DEF=Homo sapiens mRNA for KIAA0576 protein, partial cds. /FEA=mRNA /GEN=KIAA0576 /PROD=KIAA0576 protein /DB_XREF=gi:3043675 /UG-Hs.172329 KIAA0576 protein
213387_at	Consensus includes qb:AB033066.1 /DEF=Homo sapiens mRNA for KIAA1240 protein, partial cds. /FEA=mRNA /GEN=KIAA1240 /PROD=KIAA1240 Protein /DB_XREF=gi:5330790 /UG-Hs.62576 KIAA1240 protein
218143_s_at	gb:NM_005697.2 /DEF=Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA. /FEA=mRNA /GEN=SCAMP2 /PROD=secretory carrier membrane protein 2 /DB_XREF=gi:5730030 /UG-Hs.238030 secretory carrier membrane protein 2 /EL=gb:BC001376.1 qb:BC001385.1 qb:AF005038.2 qb:NM_005697.2
211615_s_at	qb:NM2439.1 /DEF=Human leucine-rich protein mRNA, complete cds. /FEA=mRNA /PROD=leucine-rich protein; leucine-rich protein /DB_XREF=gi:177109 /FL=gb:NM2439.1
213359_at	Consensus includes qb:W74620 /EST /DB_XREF=gi:1384833 /DB_XREF=est:zd77e04.s1 /CLONE=IMAGE:346686 /UG-Hs .303627 heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37kD)
217842_at	gb:NM_016019.1 /DEF=Homo sapiens CGI-74 protein (LOC51631), mRNA. /FEA=mRNA /GEN=LOC51631 /PROD=CGI-74 protein /DB_XREF=gi:7706309 /UG-Hs_.7194.1 /DEF=Homo sapiens AF151832.1 qb:NM_016019.1
202170_s_at	gb:NM_015416.1 /DEF=Homo sapiens DEFBP68AG11 protein (DKFZP586A011), mRNA. /FEA=mRNA /GEN=DKFZP586A011 /PROD=DKFZP586A011 protein
214352_s_at	Consensus includes qb:BF673699 /FEA=EST /DB_XREF=gi:119477594 /DB_XREF=est:602136427F1 /CLONE=IMAGE:4212774 /UG-Hs.184050 v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog
218287_s_at	gb:NM_012199.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2C, 1 (EIF2C1), mRNA. /FEA=mRNA /GEN=EIF2C1 /PROD=eukaryotic translation initiation factor 2C, 1 /DB_XREF=gi:6912351 /DC=Hs.14520 eukaryotic translation initiation factor 2C, 1 /FL=gb:AF093097.1 qb:NM_012199.1
204661_at	gb:NM_001803.1 /DEF=Homo sapiens antigen (CAMPATH-1 antigen) (CDW52), mRNA. /FEA=mRNA /GEN=CDW52 /PROD=CDW52 antigen (CAMPATH-1 antigen) /DB_XREF=gi:4562760 /UG-Hs.276770 CDW2 antigen (CAMPATH-1 antigen) /FL=gb:BC000644.1 qb:NM_001803.1
205545_x_at	gb:NM_014280.1 /DEF=Homo sapiens splicing factor similar to dnaj (SPF31), mRNA. /FEA=mRNA /GEN=SPF31 /PROD=splicing factor similar to dnaj /DB_XREF=gi:17657610 /UG-Hs.74711 Dnaj (Rsp40) homolog, subfamily C, member 8 /FL=gb:AF083190.1 qb:NM_014280.1
213750_at	Consensus includes qb:AB928506 /FEA=EST /DB_XREF=est:om17693.s1 /CLONE=IMAGE:1541332 /UG-Hs.10762 ESTs
221970_s_at	Consensus includes qb:AB158148 /FEA=EST /DB_XREF=gi:11019669 /DB_XREF=est:AU158148 /CLONE=PLACE:1011221 /UG-Hs.321105 Homo sapiens cDNA: ELJ21737_fis, clone COLF3395
218684_at	gb:NM_018103.1 /DEF=Homo sapiens hypothetical protein FLJ10470 (FLJ10470), mRNA. /FEA=mRNA /GEN=FLJ10470 /PROD=hypothetical protein ELJ10470 /DB_XREF=gi:8922441 /IG=Hs.44672 hypothetical protein FLJ10470 /EL=gb:NM_018103.1
200628_s_at	gb:AB61715.1 /DEF=Human tryptophanyl-tRNA synthetase (WRS) mRNA, complete cds. /FEA=mRNA /GEN=WARS /PROD=transfer RNA-Trp synthetase /DB_XREF=gi:340367 /UG-Hs.82030 tryptophanyl-tRNA synthetase /EL=gb:M77804.1 qb:NM_061715.1 qb:NM_004184.2
203905_at	gb:NM_002582.1 /DEF=Homo sapiens poly(A)-specific ribonuclease (adenylation nuclease) (PARN), mRNA. /FEA=mRNA /GEN=PARN /PROD=poly(A)-specific ribonuclease (adenylationnuclease) /DB_XREF=gi:4505610 /UG-Hs.43445 poly(A)-specific ribonuclease (adenylation nuclese) /FL=gb:NM_002582.1
204039_at	gb:NM_0043364.1 /DEF=Homo sapiens CCAATenhancer binding protein (CEBP), alpha (CEBPA), mRNA. /FEA=mRNA /GEN=CEBPA /PROD=CCAATenhancer binding protein (CEBP), alpha /DB_XREF=gi:475971 /UG-Hs.76171 CCAATenhancer binding protein (CEBP), alpha /EL=gb:NM_004364.1
63009_at	Cluster Inc. AI188402_qd08e03_x1 Homo sapiens cDNA, 3 end /clone_end=3 /gi=3739611 /ug=Hs.93391 /len=506
211922_s_at	gb:AY028632.1 /DEF=Homo sapiens catalase (CAT) mRNA, complete cds. /FEA=CDS /GEN=CAT /PROD=catalase /DB_XREF=gi:13562131 /EL=gb:AY028632.1
212861_at	Consensus includes qb:BF690150 /FEA=EST /DB_XREF=est:602186478T1 /CLONE=IMAGE:4298635 /UG-Hs.19210 ESTs

gb:NM_012252.1 /DEF=Homo sapiens transcription factor EC (TEEC), mRNA, /FEA=mRNA /GEN=TEEC /PROD=transcription factor EC	
/DB_XREF=gi:591201 /UG=Hs.113274 transcription factor EC /FI=gb:DN43945.1 qb:NM_012252.1	
213123_at	Consensus includes gi:BE222709 /FEA=EST /DB_XREF=gi:9910027 /DB_XREF=est:hu5906.x1 /CLONE=IMAGE:3173626 /UG=Hs.28785 microfibrillar-associated protein 3
204049_s_at	gb:NM_014721.1 /DEF=Homo sapiens KIAA0680 gene product /FI=gb:AB014580.1 qb:NM_014721.1 /DB_XREF=gi:1662247 /UG=Hs.102471 KIAA0680 gene product /FEA=mRNA /GEN=KIAA0680 /PROD=KIAA0680 gene product
201985_at	gb:NM_014846.1 /DEF=Homo sapiens KIAA0196 gene product /FI=gb:AB0196.1 qb:NM_014846.1 /DB_XREF=gi:8611987 /UG=Hs.8394 KIAA0196 gene product /FEA=mRNA /GEN=KIAA0196 /PROD=KIAA0196 gene product
208773_s_at	gb:ALU136943.1 /DEF=Homo sapiens CDNA DEF2p586G1024 (from clone DEF2p586G1024) complete cds. /FEA=mRNA /GEN=DKEZp586G1024 /PROD=hypothetical protein /DB_XREF=gi:12053380 /UG=Hs.301226 KIAA1085 protein /FI=gb:ALU136943.1
215953_at	gb:NM_0241633.1 /DEF=Homo sapiens hypothetical protein FLJ21276 /mRNA, /FEA=mRNA /GEN=FLJ21276 /PROD=hypothetical protein FLJ21276 /DB_XREF=gi:13315863 /UG=Hs.41502 hypothetical protein FLJ21276 /FI=gb:NM_0241633.1
218501_at	gb:NM_091555.1 /DEF=Homo sapiens Rho guanine nucleotide exchange factor (GEF) 3 (ARHGEF3), mRNA, /FEA=mRNA /GEN=ARHGEF3 /PROD=Rho guanine nucleotide exchange factor (GEF) 3 /DB_XREF=gi:9506400 /UG=Hs.25951 Rho guanine nucleotide exchange factor (GEF) 3 /FI=gb:AF249744.1 qb:NM_019555.1
212833_at	Consensus includes gb:NM_04089.1 /DEF=Human TBL gene mRNA, 3 end. /FEA=mRNA /GEN=TBL /DB_XREF=gi:182400 /UG=Hs.75639 Human TBL gene mRNA, 3 end.
209623_at	Consensus includes gb:AW39494 /FEA=EST /DB_XREF=gi:5974800 /DB_XREF=est:xt19c01.x1 /CLONE=IMAGE:2779584 /UG=Hs.167531 methylcrotonoyl-Coenzyme A carboxylase 2 (beta) /FI=gb:AB050049.1 qb:AF310971.1 qb:NM_022132.2
203969_s_at	gb:NM_0202704.1 /DEF=Homo sapiens, Similar to signal transducer and activator of transcription 1, 91kD /DB_XREF=gi:12803734 /UG=Hs.21486 signal transducer and activator of transcription 1, 91kD /PROD=similar to signal transducer and activator of transcription 1, 91kD /FI=gb:BC002704.1
219966_x_at	gb:NM_017869.1 /DEF=Homo sapiens BANP homolog, SMAR1 homolog (FLJ20538), mRNA, /FEA=mRNA /GEN=FLJ20538 /PROD=BANP homolog, SMAR1 homolog /DB_XREF=gi:8823506 /UG=Hs.194637 BANP homolog, SMAR1 homolog /FI=gb:NM_017869.1
213275_x_at	Consensus includes gb:W47179 /FEA=EST /DB_XREF=gi:13320416 /DB_XREF=est:2c34d07.s1 /CLONE=IMAGE:324205 /UG=Hs.297939 cathepsin B alpha /DB_XREF=gi:911217 /UG=Hs.145279 SET translocation (myeloid leukemia-associated) /FI=gb:D45198.1
210231_x_at	gb:DU5198.1 /DEF=Human mRNA for KIAA0241 gene, partial cds. /FEA=mRNA /GEN=KIAA0241 /DB_XREF=gi:1663699 /UG=Hs.150275 KIAA0241 protein
21212474_at	gb:BC001669.1 /DEF=Homo sapiens, Similar to oxidase (cytochrome c) assembly 1-like, clone MGC:2171, mRNA, complete cds. /FEA=mRNA /PROD=Similar to oxidase (cytochrome c) assembly 1-like /DB_XREF=gi:12804516 /UG=Hs.151134 oxidase (cytochrome c) assembly 1-like /FI=gb:BC001669.1 qb:NM_005015.1
2171527_s_at	Consensus includes gb:AA478300 /FEA=EST /DB_XREF=gi:4371526 /DB_XREF=est:tm39e01.x1 /CLONE=IMAGE:2160504 /UG=Hs.192789 ESTs, Weakly similar to ALU6 HUMAN ALU SUBELEMENT SP SEQUENCE CONTAMINATION WARNING ENTRY H. sapiens
220495_s_at	gb:NM_024715.1 /DEF=Homo sapiens hypothetical protein FLJ22625 (FLJ22625), mRNA, /FEA=mRNA /GEN=FLJ22625 /PROD=transformer 2 Drosophila homolog 10, clone MGC:0454, mRNA, complete factor, argininoserine-rich (transformer 2 Drosophila homolog 10) /FI=gb:BC00160.1 qb:EC000451.1 qb:NM_005593.1
202529_at	gb:NM_013451.1 /DEF=Homo sapiens fer-1 (C. elegans)-like 3 (myoferlin) (FER1L3), mRNA, /FEA=mRNA /GEN=FER1L3 /PROD=fer-1 (C. elegans)-like 3 (myoferlin) /DB_XREF=gi:7303052 /UG=Hs.234680 fer-1 (C. elegans)-like 3 (myoferlin) /FI=gb:AF182316.1 qb:NM_013451.1
200892_s_at	gb:BC000451.1 /DEF=Homo sapiens, splicing factor, argininoserine-rich (transformer 2 Drosophila homolog 10) /FI=gb:BC000451.1 qb:NM_005035, splicing factor, argininoserine-rich (transformer 2 Drosophila homolog 10) /DB_XREF=gi:12653362 /UG=Hs.30035
201798_s_at	gb:NM_013451.1 /DEF=Homo sapiens fer-1 (C. elegans)-like 3 (myoferlin) (FER1L3), mRNA, /FEA=mRNA /GEN=FER1L3 /PROD=fer-1 (C. elegans)-like 3 (myoferlin) /DB_XREF=gi:7303052 /UG=Hs.234680 fer-1 (C. elegans)-like 3 (myoferlin) /FI=gb:AF182316.1 qb:NM_013451.1
2008897_s_at	gb:NM_002766.1 /DEF=Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA, /FEA=mRNA /PROD=phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA, /FEA=mRNA /GEN=PRPSAP1 /PROD=phosphoribosyl pyrophosphate synthetase-associated protein 1 /DB_XREF=gi:4506130 /UG=Hs.77498 phosphoribosyl pyrophosphate synthetase-associated protein 1 /FI=gb:D61391.1 qb:NM_002766.1
210296_s_at	gb:BC003360.1 /DEF=Homo sapiens, DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myo-regulated), clone MGC:5316, mRNA, complete cds. /FEA=mRNA /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 18 (Myo-regulated) /FI=gb:BC003360.1
2008897_s_at	gb:BC005375.1 /DEF=Homo sapiens, peroxisomal membrane protein 3 (35kd, Zellweger syndrome), clone MGC:12491, mRNA, complete cds. /FEA=mRNA /PROD=peroxisomal membrane protein 3 (35kd, Zellweger syndrome) /FI=gb:BC005375.1
212460_at	Consensus includes gb:BE738425 /FEA=EST /DB_XREF=gi:10152417 /DB_XREF=est:60157244171 /CLONE=IMAGE:38393147 /UG=Hs.241507 ribosomal protein S6

211800_s_at	gb:AE017306.1 /DBF=Homo sapiens deubiquitinating enzyme UspS (UNP) mRNA, complete cds. /FEA=mRNA /PROD=Unp /DB_XREF=gi:2656142 /UG=Hs.77500 ubiquitin specific protease 4 (proto-oncogene) /Fl=gb:AE017306.1
202850_at	gb:NM_002858.2 /DBF=Homo sapiens AtP-binding cassette, sub-family D (ALD), member 3 (ABCD3) , mRNA. /FEA=mRNA /GEN=ABCD3 /PROD=ATP-binding cassette, sub-family D (ALD), member 3 /DB_XREF=gi:10947125 /UG=Hs.76781 AtP-binding cassette, sub-family D (ALD), member 3 /Fl=gb:NM_002858.2 /gb:NM_081186.1 Consensus includes gb:DB_XREF=est:602542252F1 /CLONE=IMAGE:4673316 /UG=Hs.16492 DKFZP564G2022 protein
212202_s_at	gb:JAF063020.1 /DBF=Homo sapiens lens epithelium-derived growth factor mRNA, complete cds. /FEA=mRNA /PROD=lens epithelium-derived growth factor /DB_XREF=gi:283351 /UG=Hs.82110 PC4 and SER1 interacting protein 1 /Fl=gb:NM_021144.1 /gb:AF0503020.1
207616_s_at	gb:NM_004180.1 /DBF=Homo sapiens TRAF family member-associated NFKB activator (TANK) , mRNA. /FEA=mRNA /GEN=TANK /PROD=TRAF Family member-associated NFKB activator /Fl=gb:U53830.1 /gb:NM_004180.1
204630_s_at	gb:NM_004871.1 /DBF=Homo sapiens golgi SNAP receptor complex member 1 (GORSL1) , mRNA. /FEA=mRNA /GEN=GORSL1 /PROD=golgi SNAP receptor complex member 1 /Fl=gb:AE073926.1 /gb:NM_004871.1
209422_at	Consensus includes gb:AI109865 /DEF=Human DNA sequence from clone RP5-1121G12 on chromosome 20 Contains the 3' end of a gene encoding two isoforms (the hepatocellular carcinoma-associated antigen 58 (HCA58) and a putative novel protein containing a PHD finger domain), the SCAND1 gene... /FEA=mRNA 2 /DB_XREF=gi:112594 hypothetical protein DKEZP434F0272 /Fl=gb:AY07523.1 /gb:AF348207.1
203658_at	gb:BG001689.1 /DBF=Homo sapiens carnitineacylcarnitine translocase, Clone MGC:1207, mRNA, complete cds. /FEA=mRNA /PROD=carnitineacylcarnitine translocase /DB_XREF=gi:12804552 /UG=Hs.13845 solute carrier family 25 (carnitineacylcarnitine translocase), member 20 /Fl=gb:BC001689.1 /gb:NM_000381.2 Consensus includes gb:BF690062 /FEA=EST /DB_XREF=gi:111975470 /DB_XREF=est:602186366T1 /CLONE=IMAGE:4298440 /UG=Hs.172550 polyuridylic acid binding protein (heterogeneous nuclear ribonucleoprotein I)
222122_s_at	Consensus includes gb:BG403671 /FEA=EST /DB_XREF=gi:13297119 /DB_XREF=est:602419393F1 /CLONE=IMAGE:45263326 /UG=Hs.16411 hypothetical protein LOC57187 Consensus includes gb:AI146275 /FEA=EST /DB_XREF=est:AU146275 /CLONE=HEMB1000004 /UG=Hs.6557 zinc finger protein 161 /Fl=gb:ID28118.1 /gb:NM_007116.1
210460_s_at	gb:AB033605.1 /DEF=Homo sapiens mRNA for PIB-R5, complete cds. /FEA=mRNA /GEN=hpib-R5 /PROD=pub-R5 /DB_XREF=gi:8918332 /UG=Hs.148495 protein (prosome, macropain) 26S subunit, non-APase, 4 /Fl=gb:AB033605.1
207551_s_at	gb:NM_006800.1 /DBF=Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1) , tRNA. /FEA=mRNA /GEN=MSL3L1 /PROD=male-specific lethal-3 (Drosophila)-like 1 /Fl=gb:AF11065.1 /gb:NM_006800.1
201104_x_at	gb:NM_015383.1 /DBF=Homo sapiens hypothetical protein (D328E19.11), mRNA. /FEA=mRNA /GEN=D328E19.C1.1 /PROD=hypothetical protein /DB_XREF=gi:7657016 /UG=Hs.218339 hypothetical protein /Fl=gb:NM_015383.1
200812_at	gb:NM_006429.1 /DBF=Homo sapiens chaperonin containing TCP1, subunit 7 (eta) (CCT7) , mRNA. /FEA=mRNA /GEN=CCT7 /PROD=chaperonin containing TCP1, subunit 7 (eta) /DB_XREF=gi:15453606 /UG=Hs.108809 chaperonin containing TCP1, subunit 7 (eta) /Fl=gb:AF026592.1 /gb:NM_006129.1
203494_s_at	gb:NM_014679.1 /DBF=Homo sapiens KIAA0092 gene product (KIAA0092) , mRNA. /FEA=mRNA /GEN=KIAA0092 /PROD=KIAA0092 gene product /DB_XREF=gi:7661899 /UG=Hs.151791 KIAA0092 gene product /Fl=gb:ID2054.1 /gb:NM_014679.1
202127_at	Consensus includes gb:AB011108.1 /DEF=Homo sapiens kinase PRP4 homolog /Fl=gb:ID148736.1 /gb:NM_003913.1 /DB_XREF=gi:3043595 /UG=Hs.198831 serine/threonine-protein kinase PRP4 homolog /Fl=gb:ID148736.1 /gb:NM_003913.1
212532_s_at	Consensus includes gb:AW873564 /FEA=EST /DB_XREF=gi:8007617 /DB_XREF=est:ho62c10.x1 /CLONE=IMAGE:3041970 /UG=Hs.155485 huntingtin interacting protein 2 /gb:NM_012459.1 /DBF=Homo sapiens translocase of inner mitochondrial membrane 8 (yeast) homolog B (TIM8B1) , mRNA. /FEA=mRNA /GEN=TIM8B1 /PROD=translocase of inner mitochondrial membrane 8 (yeast) homolog B /DB_XREF=gi:6912711 /UG=Hs.279915 translocase of inner mitochondrial membrane 8
218357_s_at	(yeast) homolog B /Fl=gb:AF150087.1 /gb:AE152350.1 /gb:NM_012459.1 /gb:NM_012459.1 /DEF=Human alcohol dehydrogenase class III (ADH5) mRNA, complete cds. /FEA=mRNA /GEN=ADH5 /DB_XREF=gi:178131 /UG=Hs.78989 alcohol dehydrogenase 5 (class III), chi polypeptide /Fl=gb:NM_000671.2 /gb:NM_029872.1 /gb:NM_029872.1
207730_x_at	gb:NM_017932.1 /DEF=Homo sapiens hypothetical protein FLJ20700 (FLJ20700) , mRNA. /FEA=mRNA /GEN=FLJ20700 /PROD=hypothetical protein FLJ20700 /DB_XREF=gi:5923629 /UG=Hs.272222 hypothetical protein FLJ20700 /Fl=gb:NM_017932.1
212896_at	Consensus includes gb:D29641.2 /DBF=Homo sapiens mRNA for KIAA0052 protein /DB_XREF=gi:6633994 /UG=Hs.278608 KIAA0052 protein /DB_XREF=gi:6633994 /UG=Hs.278608 KIAA0052 protein
203156_at	gb:NM_016248.1 /DBF=Homo sapiens A-kinase anchoring protein 220 (LOC51707) , mRNA. /FEA=mRNA /GEN=LOC51707 /PROD=A-kinase anchoring protein 220 /DB_XREF=gi:71706456 /UG=Hs.232076 A kinase (PRKA) anchor protein 11 /Fl=gb:AF176555.1 /gb:NM_016248.1
220666_at	gb:NM_022162.1 /DBF=Homo sapiens NOD2 protein (NOD2) , mRNA. /FEA=mRNA /GEN=NOD2 /PROD=NOD2 protein /DB_XREF=gi:11545911 /UG=Hs.135201 NOD2 protein /Fl=gb:AF178910.1 /gb:NM_022162.1

protein /FL=gb:AF178930.1 gb:NM_022162.1	gb:NM_020640.1 /DEF=Homo sapiens RP42 homolog (RP42), mRNA. /FEA=mRNA /GEN=RP42 /PROD=RP42 homolog /DB_XREF=gi:10190677 /UG=Hs.104613 RP42 homolog /FL=gb:NM_020640.1 gb:AF292100.2
221689_s_at	gb:AB035745.1 /DEF=Homo sapiens mRNA for DSCR5b, complete cds. /FEA=mRNA /GEN=DSCR5b /PROD=DSCR5b /DB_XREF=gi:17798596 /UG=Hs.66493 Down syndrome critical region gene 5 /EL=gb:AB035745.1 gb:AB037163.1 gb:AF237812.1
205412_at	gb:NM_000019.1 /DEF=Homo sapiens acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A acetyltransferase 1 precursor /DB_XREF=gi:1557236 /UG=Hs.37 mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACAT1 /PROD=acetyl-Coenzyme A acetyltransferase 1 precursor /DB_XREF=gi:1557236 /UG=Hs.37
202542_s_at	gb:NM_004757.1 /DEF=Homo sapiens small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating factor 1 (endothelial monocyte-activating) (SCYE1), mRNA. /FEA=mRNA /GEN=SCYE1 /PROD=CCMC-binding factor (zinc finger protein) (CCMC1), mRNA. /FEA=mRNA /GEN=CCMC /PROD=CCMC-binding factor (zinc finger protein) /EL=gb:NM_000019.1
202521_at	gb:NM_006565.1 /DEF=Homo sapiens CCCTC-binding factor (zinc finger protein) (CCTC1), mRNA. /FEA=mRNA /GEN=CCTC /PROD=CCTC-binding factor (zinc finger protein) /EL=gb:NM_006565.1 gb:AF25435.1
201391_x_at	gb:NM_015905.1 /DEF=Homo sapiens transcriptional intermediary factor 1 (TIF1), mRNA. /FEA=mRNA /GEN=TIF1 /PROD=transcriptional intermediary factor 1 alpha /DB_XREF=gi:7706233 /UG=Hs.183858 transcriptional intermediary factor 1 /EL=gb:AF009353.1 gb:AF119042.1 gb:NM_003852.1
214733_s_at	Consensus includes gb:AF031427 /DEF=Human DNA sequence from clone 167a19 on chromosome 1p32.1-33. Contains three genes for novel proteins, the D10L gene for type I iodotyrosine deiodinase (EC 3.8.1.4, TXR1, ITD1) and an MRNRP A3 (Heterogenous Nuclear Ribonucleoprotein A3, FBRNP) ... /FEA=mRNA 6 /DB_XREF=gi:483258 /UG=Hs.11923 hypothetical protein
217864_s_at	gb:NM_016166.1 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspH1) box binding protein 1 (DDXBP1), mRNA. /FEA=mRNA /GEN=DDXBP1 /PROD=DDXBP1 (Asp-Glu-Ala-AspH1) box binding protein 1 /DB_XREF=gi:17706636 /UG=Hs.75251 DEAH (Asp-Glu-Ala-AspH1) box binding protein 1 /EL=gb:AF07951.1
212904_at	Consensus includes gb:AB033011.1 /DEF=Homo sapiens mRNA for KIAA1185 protein, partial cds. /FEA=mRNA /GEN=KIAA1185 /PROD=KIAA1185 protein /DB_XREF=gi:3330301 /UG=Hs.268488 KIAA1185 protein
202126_at	Consensus includes gb:AA156948 /DB_XREF=est:gi:11728563 /DB_XREF=est:119f02.s1 /CLONE=IMAGE:502395 /UG=Hs.198891 serinethreonine-protein kinase PRP4 homolog /FL=gb:U487336.1 gb:NM_003913.1
203484_at	gb:NM_014302.1 /DEF=Homo sapiens Sec61 gamma (SEC61G), mRNA. /FEA=mRNA /GEN=SEC61G /PROD=Sec61 gamma /DB_XREF=gi:1.7657545 /UG=Hs.9950 Sec61 gamma /FL=gb:AF054184.1 gb:NM_014302.1
203345_s_at	Consensus includes gb:AB156096 /FEA=EST /DB_XREF=gi:4524548 /DB_XREF=est:tn53d02.x1 /CLONE=IMAGE:2172099 /UG=Hs.31016 putative DNA binding protein /EL=gb:AF072814.1 gb:NM_007358.1
213238_at	Consensus includes gb:AF478147 /FEA=EST /DB_XREF=gi:4371373 /DB_XREF=est:tm34f06.x1 /CLONE=IMAGE:2160035 /UG=Hs.173540 ATPase, Class V, type 10D
202680_at	gb:NM_002005.1 /DEF=Homo sapiens general transcription factor III, polypeptide 2 (beta subunit, 34kd) (GTF2E2), mRNA. /FEA=mRNA /GEN=GTF2E2 /PROD=general transcription factor III, polypeptide 2 (beta subunit, 34kd) /DB_XREF=gi:4504194 /UG=Hs.77100 general transcription factor III, polypeptide 2 (beta subunit, 34kd) /FL=gb:NM_002005.1
218117_at	gb:NM_014248.1 /DEF=Homo sapiens ring-box 1 (RBX1), mRNA. /FEA=mRNA /GEN=RBX1 /PROD=ring-box 1 /DB_XREF=gi:17657507 /UG=Hs.279919 ring-box 1 /FL=gb:BC001466.1 gb:AF140598.1 gb:AF42039.1 gb:NM_014248.1
218768_at	gb:NM_020401.1 /DEF=Homo sapiens nuclear pore complex protein (NUF107), mRNA. /FEA=mRNA /GEN=NUF107 /PROD=nuclear pore complex protein /DB_XREF=gi:1.996680 /UG=Hs.236204 nuclear pore complex protein /FL=gb:NM_020401.1
202271_at	Consensus includes gb:AB007952.1 /DEF=Homo sapiens mRNA for KIAA0483 protein, partial cds. /FEA=mRNA /GEN=KIAA0483 /PROD=KIAA0483 protein /DB_XREF=gi:1.3413925 /UG=Hs.64691 KIAA0483 protein /FL=gb:NM_015176.1
218543_s_at	gb:NM_022750.1 /DEF=Homo sapiens hypothetical protein FLJ22693 (FLJ22693), mRNA. /FEA=mRNA /GEN=FLJ22693 /PROD=hypothetical protein FLJ22693 /DB_XREF=gi:12239412 /UG=Hs.12646 hypothetical protein FLJ22693 /FL=gb:AU156766.1 gb:NM_022750.1
203146_s_at	gb:NM_001410.1 /DEF=Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 1, mRNA. /FEA=mRNA /GEN=GABBR1 /PROD=gamma-aminobutyric acid (GABA) B receptor, 1 /FL=gb:NM_001410.1 gb:AF301005.1 gb:AF099148.1
218140_x_at	gb:NM_021203.1 /DEF=Homo sapiens APMCFL protein (APMCFL), mRNA. /FEA=mRNA /GEN=APMCFL /PROD=APMCFL protein /DB_XREF=gi:10864014
10420_at	Cluster Incl. AB015718:Homo sapiens 10k mRNA for protein kinase, complete cds /cds:150_2956 /gb:AB015718 /gi:4001687 /ug:hs.16134 /len=4221

209371_x_at	Consensus includes gb:AI928526 /DB_XREF=g1:15664490 /DB_XREF=est:wp59a06.x1 /CLONE=IMAGE:2466034 /UG-Hs.259730 home-regulated initiation factor 2-alpha kinase /FL=gb:AE116615.1
48550_at	Cluster IncI_05577_HsU5577 Homo sapiens cDNA /clone=27698 /gb=U55777 /gb=g1:1334513 /gb=Hs.180333 /len=1593
202416_at	gb:NM_003315.1 /DEF=Homo sapiens tetratricopeptide repeat domain 2 (TTC2), mRNA, /FEA=mRNA /GEN=tTC2 /PROD=tetratricopeptide repeat domain 2 /DB_XREF=g1:4507712 /UG-Hs.5542 DnaJ (Hsp10) homolog, subfamily C, member 7 /FL=gb:U6571.1 qb:NM_003315.1
211727_g_at	gb:BC00595.1 /DEF=Homo sapiens Cox11 (yeast) homolog, cytochrome c oxidase assembly protein, clone MGC:14469, mRNA, complete cds. /FEA=mRNA /PROD=COX11 (yeast) homolog, cytochrome c oxidase assembly protein /DB_XREF=g1:13343414 /FL=gb:BC00595.1
202125_s_at	gb:NM_01049.1 /DEF=Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome 3 /DB_XREF=g1:13027319 /UG-Hs.154248 amyotrophic lateral sclerosis 2 (juvenile) chromosome 3 /candidate 3 /FL=gb:AB038931.1 qb:NM_015049.1
209451_at	gb:U59863.1 /DEF=Ruman TRAF-Interacting protein 1-TRAF mRNA, complete cds. /FEA=mRNA /PROD=I-TRAF /DB_XREF=g1:1518017 /UG-Hs.146847 TRAF family member-associated NERB activator /FL=gb:U59863.1
209440_at	gb:BC00105.1 /DEF=Homo sapiens phosphoribosyl pyrophosphate synthetase 1 /DB_XREF=g1:12804406 /UG-Hs.56 phosphoribosyl pyrophosphate synthetase 1 /FEA=mRNA /PROD=phosphoribosyl pyrophosphate synthetase 1 /FL=gb:BC00105.1
218189_s_at	gb:NM_018946.2 /DEF=Homo sapiens N-acetylneuraminic acid phosphate synthase; sialic acid synthase (SAS), mRNA, /FEA=mRNA /GEN=SAS /PROD=N-acetylneuraminic acid phosphate synthase; sialic acid synthase /FL=gb:NM_018946.2 qb:BC000008.1 qb:AC257466.1
200947_s_at	gb:NM_002271.1 /DEF=Homo sapiens glutamate dehydrogenase 1 (GLUD1), mRNA, /FEA=mRNA /GEN=GLUD1 /PROD=glutamate dehydrogenase 1 /DB_XREF=g1:4885380 /UG-Hs.77508 glutamate dehydrogenase 1 /FL=gb:U03248.1 qb:NM37154.1 qb:M20867.1 qb:NM_005271.1
202798_at	gb:NM_005323.1 /DEF=Homo sapiens SEC24 (S. cerevisiae) related gene family, member B (SEC24B), mRNA, /FEA=mRNA /GEN=SEC24B /PROD=SEC24 (S. cerevisiae) related gene family, member B /DB_XREF=g1:5454045 /UG-Hs.7239 SEC24 (S. cerevisiae) related gene family, member B /FL=gb:NM_005323.1
205323_s_at	gb:NM_00955.1 /DEF=Homo sapiens metal-regulatory transcription factor 1 (MTF1), mRNA, /FEA=mRNA /GEN=MTF1 /PROD=metal-regulatory transcription factor 1 /DB_XREF=g1:5174588 /UG-Hs.21158 metal-regulatory transcription factor 1 /FL=gb:NM_00955.1
212622_at	Consensus includes gb:NM4760 /FEA=EST /DB_XREF=g1:1212589 /CLONE=IMAGE:y30c06.s1 /UG-Hs.174905 KIAA0033 protein
212033_at	Consensus includes gb:BF055107 /FEA=EST /DB_XREF=g1:10809003 /DB_XREF=est:j77a05.x1 /CLONE=IMAGE:3392240 /UG-Hs.180789 S164 protein /FL=gb:NM_005323.1
218919_at	gb:NM_024699.1 /DEF=Homo sapiens hypothetical protein FLJ14007, mRNA, /FEA=mRNA /GEN=FLJ14007 /PROD=hypothetical protein FLJ14007 /DB_XREF=g1:13375984 /UG-Hs.99519 hypothetical protein FLJ14007 /FL=gb:NM_024699.1
202971_at	gb:AB032251.1 /DEF=Homo sapiens BPF1 mRNA, for bromodomain PHD finger transcription factor /DB_XREF=g1:6833491 /UG-Hs.99872 fetal Alzheimer antigen /FL=gb:AB032251.1 /PROD=bromodomain PHD finger transcription factor /DB_XREF=g1:6833491 /UG-Hs.99872 fetal Alzheimer antigen /FL=gb:AB032251.1
213322_at	Consensus includes gb:AL031778 /DEF=Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel benzodiazapine receptor with ZU5 domain similar to part of Tight Junction Protein 201 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine... /FEA=mRNA 2 /DB_XREF=g1:4153958 /UG-Hs.183056 Human DNA sequence from clone 31B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein 201 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine receptor
221895_at	Consensus includes gb:AM469184 /FEA=EST /DB_XREF=est:hc789504.x1 /CLONE=IMAGE:2898870 /UG-Hs.65406 ESTs
217760_at	Consensus includes gb:AA1176780 /FEA=EST /DB_XREF=g1:1757929 /DB_XREF=est:zp32a10.s1 /CLONE=IMAGE:611130 /UG-Hs.14512 DIPB protein /FL=gb:NM_017583.1
201448_at	Consensus includes gb:AL046419 /FEA=EST /DB_XREF=g1:5434493 /DB_XREF=est:DKFZP434N247_s1 /CLONE=DKFZP434N247 /UG-Hs.239469 TIA1 cytotoxic granule-associated RNA-binding protein /FL=gb:NM_022037.1 qb:MT7142.1
218465_at	gb:NM_018126.1 /DEF=Homo sapiens hypothetical protein FLJ10525 (FLJ10525), mRNA, /FEA=mRNA /GEN=FLJ10525 /PROD=hypothetical protein FLJ10525 /DB_XREF=g1:8922490 /UG-Hs.31082 hypothetical protein FLJ10525 /FL=gb:BC000948.1 qb:NM_018126.1
212880_at	Consensus includes gb:AB011113.1 /DEF=Homo sapiens mRNA for KIAA0541 protein, partial cds. /FEA=mRNA /GEN=KIAA0541 /PROD=KIAA0541 protein /DB_XREF=g1:3043605 /UG-Hs.10881 WD repeat domain 7
218142_s_at	gb:NM_016302.1 /DEF=Homo sapiens protein x 0001 (LOC51185), mRNA, /FEA=mRNA /GEN=LOC51185 /PROD=protein x 0001 /DB_XREF=g1:10047097 /UG-Hs.18925 protein x 0001 /FL=gb:NM_016302.1 qb:AF117230.1
202078_at	gb:NM_003653.1 /DEF=Homo sapiens COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 3 (COP9S1), mRNA, /FEA=mRNA /GEN=COP9S1 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 3 /DB_XREF=g1:4502974 /UG-Hs.6076 COP9 (constitutive photomorpho-

212345_s_at	Consensus includes gb:BE675139 / FEA=EST / DB_XREF=gi:10035680 / DB_XREF=est:7f03b12.x1 / CLONE=IMAGE:3293567 / 0G-Hs.13659 hypothetical protein DKFZ586T2423
213982_s_at	Consensus includes gb:BG107203 / FEA=EST / DB_XREF=gi:12601049 / DB_XREF=est:602290933F1 / CLONE=IMAGE:4385577 / 0G-Hs.242271 KIAA0471 gene product
202519_at	gb:NM_014938.1 / DEF=Homo sapiens KIAA0867 protein (MONDOA), mRNA. / FEA=mRNA / GEN=MONDOA / PROD=MondoA protein / DB_XREF=gi:7662347 /UG-Hs.52081 KIAA0867 protein /EL=gb:AB020674.1 qb:NM_014938.1
202892_at	gb:NM_004661.1 / DEF=Homo sapiens CDC23 (cell division cycle 23, yeast homolog) (CDC23), mRNA. / FEA=mRNA / GEN=CDC23 / PROD=cell division cycle 23, yeast homolog / CDC23 / DB_XREF=gi:4757947 /UG-Hs.153546 CDC23 (cell division cycle 23, yeast, homolog) / EL=gb:AF053977.1
213876_x_at	gb:AB011472.1 qb:NM_004661.1 qb:AF191341.1
	consensus includes gb:AW089584 / FEA=EST / DB_XREF=gi:6046928 / DB_XREF=est:xd2f04.x1 / CLONE=IMAGE:2591335 /UG-Hs.171909 U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2
202054_s_at	gb:NM_000382.1 / DEF=Homo sapiens aldehyde dehydrogenase 3 family, member A2 (ALDH3A2), mRNA. / FEA=mRNA / GEN=ALDH3A2 / PROD=aldehyde dehydrogenase 3A2 / DB_XREF=gi:4557302 /UG-Hs.15908 aldehyde dehydrogenase 3 family, member A2 / EL=gb:L47162.1 qb:NM_000382.1
211776_at	gb:AF167438.1 / DEF=Homo sapiens androgen-regulated short-chain dehydrogenase/reductase 1 (ARDSR1) mRNA, complete cds. / FEA=mRNA / GEN=ARDSR1 /PROD=androgen-regulated short-chain dehydrogenase/reductase 1 / DB_XREF=gi:9622123 /UG-Hs.179817 CCG-82 protein /EL=gb:BC000112.1
208758_at	gb:DB89976.1 / DEF=Homo sapiens mRNA for 5-aminoimidazole-4-carboxamide ribonucleotide transformylase, complete cds. / FEA=mRNA / PROD=5-aminoimidazole-4-carboxamide ribonucleotide transformylase /DB_XREF=gi:2317691 /UG-Hs.90280 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase IMP cyclohydrolase /EL=gb:U77436.1 qb:DB89976.1 qb:NM_004044.1
2121749_s_at	Consensus includes gb:AU096477 / FEA=EST / DB_XREF=gi:3443971 / DB_XREF=est:qa03C06.x1 / CLONE=IMAGE:1685674 /UG-Hs.48297 DKEZP586C1620 protein
200890_s_at	Consensus includes gb:AU006345 / FEA=EST / DB_XREF=gi:5855123 / DB_XREF=est:wt04d05.x1 / CLONE=IMAGE:2506473 /UG-Hs.250773 signal sequence receptor, alpha (transcoxon-associated protein alpha) / EL=gb:AF156965.1 qb:NM_003144.2
2111675_s_at	gb:AF051589.1 / DEF=Homo sapiens HIC Protein isoform p40 and HIC protein isoform p32 mRNAs, complete cds. / FEA=mRNA / PROD=HIC protein isoform p32; HIC protein isoform p40 /DB_XREF=gi:3426297 / EL=gb:AE051589.1
206792_x_at	gb:NM_000923.1 / DEF=Homo sapiens phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1) (PDE4C), mRNA, / FEA=mRNA / GEN=PDE4C / PROD=phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1) / DB_XREF=gi:4505654 /UG-Hs.189 phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1) / EL=gb:NM_000923.1
21218710_at	gb:NM_016205.1 / DEF=Homo sapiens platelet derived growth factor C (PDGFC), mRNA, / FEA=mRNA / GEN=PDGFC / PROD=secretory growth factor-like protein fallotene /DB_XREF=gi:9994186 /UG-Hs.43080 platelet derived growth factor C / EL=gb:AE091434.1 qb:AE244813.1 qb:NM_003831.1 qb:NM_016205.1
201742_x_at	gb:NM_006924.1 / DEF=Homo sapiens splicing factor, argininoserine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), mRNA. / FEA=mRNA / GEN=SFRS1 / PROD=splicing factor, argininoserine-rich 1 (splicing factor 2, alternate splicing factor) /DB_XREF=gi:5902075 /UG-Hs.73737 splicing factor, argininoserine-rich 1 (splicing factor 2, alternate splicing factor) /EL=gb:MS9040.1 qb:NM_006924.1
20218622_at	gb:NM_024057.1 / DEF=Homo sapiens hypothetical protein MGCS585 (MGCS585), mRNA. / FEA=mRNA / GEN=MGCS585 / PROD=hypothetical protein MGCS585 / DB_XREF=gi:13120207 /UG-Hs.5152 hypothetical protein MGCS585 / EL=gb:BC000861.1 qb:NM_024057.1
21212176_at	Consensus includes gb:AP092326 / FEA=EST / DB_XREF=gi:3037233 / DB_XREF=est:ox92b01.s1 / CLONE=IMAGE:1521385 /UG-Hs.18368 DKEZP586B0769 protein
2128970_s_at	gb:NM_015986.1 / DEF=Homo sapiens CGI-32 protein (LOC51076), mRNA. / FEA=mRNA / GEN=LOC51076 / PROD=CGI-32 protein /DB_XREF=gi:7705727 /UG-Hs.162326.1 / DEF=Homo sapiens splicing factor, argininoserine-rich 4 (SFRS4), mRNA. / FEA=mRNA / GEN=SFRS4 / PROD=splicing factor, argininoserine-rich 4 / DB_XREF=gi:5032088 /UG-Hs.76122 splicing factor, argininoserine-rich 4 / EL=gb:BC002781.1 qb:Li4076.1 qb:NM_005626.1
2222103_at	Consensus includes gb:AF143345 / FEA=EST / DB_XREF=gi:4295529 / DB_XREF=est:ti48086.x1 / CLONE=IMAGE:2133683 /UG-Hs.36908 activating transcription factor 1 / EL=gb:NM_005171.1
2040436_at	Consensus includes gb:AW269335 / FEA=EST / DB_XREF=gi:6656365 /DB_XREF=est:xs47d05.x1 / CLONE=IMAGE:2727277 /UG-Hs.75194 endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 2, / EL=gb:U78192.1 qb:NM_001401.1
2118283_at	gb:NM_016305.1 / DEF=Homo sapiens Kaa-iso protein (LOC51188), mRNA. / FEA=mRNA / GEN=LOC51188 / PROD=Kaa-iso protein /DB_XREF=gi:10047103 /UG-Hs.9774 Kaa-iso protein /EL=gb:NM_016305.1 qb:AF201950.1
209654_at	gb:NM_5070 KAA0947 protein / FEA=mRNA / GEN=KAA0947 / PROD=Unknown (protein for MGC:4271) / DB_XREF=gi:13336178

209083_at	gb:U34690.1 /DEF=Human coronin-like protein (HCOR01) mRNA, complete cds. /FEA=mRNA /GEN=HCOR01 /PROD=coronin-like protein /DB_XREF=gi:1002932 /UG=Hs.109606 coronin, actin-binding protein, 1A /FL=gb:U34690.1 qb:NM_007044.1 qb:D44497.1
221873_at	Consensus includes gb:AW62015 /FEA=EST /DB_XREF=gi:6301048 /DB_XREF=est:au72d09.x1 /CLONE=IMAGE:2781809 /UG=Hs.154095 zinc finger protein 1A3 (Clone pHZ-1)
213573_at	Consensus includes gb:AA861608 /FEA=EST /DB_XREF=gi:2953748 /DB_XREF=est:ak34e01.s1 /CLONE=IMAGE:1407864 /UG=Hs.180446 karyopherin (importin) beta 1 gb:AF114784.1 /DEF=Homo sapiens methyl-CG binding endonuclease (MED1) mRNA, complete cds. /FEA=mRNA /GEN=MED1 /PROD=methyl-CG binding endonuclease /DB_XREF=gi:1453975B /UG=Hs.35947 methyl-CG binding domain protein 4 /FL=gb:AE072205.1 qb:NM_003925.1 qb:AF114784.1
219097_x_at	gb:NM_024104.1 /DEF=Homo sapiens hypothetical protein MGC2747 (MGC2747) mRNA. /FEA=mRNA /GEN=MGC2747 /PROD=hypothetical protein MGC2747 /DB_XREF=gi:13129111 /UG=Hs.227203 hypothetical protein MGC2747 /FL=gb:BC001680.1 qb:BC001948.1 qb:NM_024104.1
206513_at	gb:NM_004833.1 /DEF=Homo sapiens absent in melanoma 2 (AIM2) mRNA. /FEA=mRNA /GEN=AIM2 /PROD=absent in melanoma 2 /DB_XREF=gi:4757733 /UG=Hs.101615 absent in melanoma 2 /FL=gb:AE024714.1 qb:NM_004833.1 gb:AF165513.1 /DEF=Homo sapiens vacuolar protein sorting 45 isoform (VPS45) mRNA, complete cds. /FEA=mRNA /GEN=VPS45 /PROD=vacuolar protein sorting 45 isoform /DB_XREF=gi:929432 /UG=Hs.6550 vacuolar protein sorting 45B (yeast homolog) /FL=gb:NM_007259.1 qb:AF165513.1 gb:NM_016085.1 /DEF=Homo sapiens apoptosis related protein APR-3 (APR-3) mRNA. /FEA=mRNA /GEN=APR-3 /PROD=apoptosis related protein APR-3
209268_at	DB_XREF=gi:7706360 /UG=Hs.9527 apoptosis related protein APR-3 /FL=gb:AE144055.2 qb:NM_016085.1 /DB_XREF=gi:005095.1 /DEF=Homo sapiens zinc finger protein 262 (ZNF262) mRNA. /FEA=mRNA /GEN=ZNF262 /PROD=zinc finger protein 262 /DB_XREF=gi:4827068 /
200749_at	US=Rs.150390 zinc finger protein 262 /FL=gb:AB007885.1 qb:NM_005095.1 Consensus includes gb:BF112006 /FEA=EST /DB_XREF=gi:10941619 /DB_XREF=est:7137e05.x1 /CLONE=IMAGE:3523665 /UG=Hs.10842 RAN, member RAS oncogene family /
219329_s_at	FL=gb:BC000832.1 qb:BC004272.1 qb:AE052578.1 qb:NM_006325.2 Consensus includes gb:BF139983 /FEA=EST /DB_XREF=gi:11452500 /DB_XREF=est:nac5111.x1 /CLONE=IMAGE:3406220 /UG=Hs.19949 caspase 8, apoptosis-related cysteine protease /FL=gb:U58143.1
212673_at	Consensus includes gb:D42084.1 /DEF=Human mRNA for KIAA0094 gene, partial cds. /FEA=mRNA /GEN=KIAA0094 /DB_XREF=gi:577314 /UG=Hs.82007 KIAA0094 protein
201771_at	gb:NM_005698.1 /DEF=Homo sapiens secretory carrier membrane protein 3 (SCAMP3) mRNA. /FEA=mRNA /GEN=SCAMP3 /PROD=secretory carrier membrane protein 3 /FL=gb:BC000161.2 qb:BC005135.1 qb:AF05039.1 /gb:NM_005698.1
209607_x_at	gb:008032.1 /DEF=Human thermolabile (monoamine, N form) phenol sulfotransferase (STM) mRNA, complete cds. /FEA=mRNA /GEN=STM /PROD=thermolabile (monoamine, N form) phenol sulfotransferase /DB_XREF=gi:4682256 /UG=Hs.274614 sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3 /FL=gb:NM_003166.1 qb:U34199.1 qb:108032.1
217317_s_at	Consensus includes gb:AB002391.2 /DEF=Homo sapiens mRNA for KIAA0393 protein, partial cds. /FEA=mRNA /GEN=KIAA0393 /PROD=KIAA0393 protein /DB_XREF=gi:6683656 /UG=Hs.266933 hect domain and RLD 2
202272_s_at	gb:NM_015176.1 /DEF=Homo sapiens protein KIAA0483 mRNA. /FEA=mRNA /GEN=KIAA0483 /PROD=KIAA0483 protein /DB_XREF=gi:17662157 /UG=Hs.64691 KIAA0483 protein /FL=gb:NM_015176.1
210629_x_at	gb:AE000425.1 /DEF=Homo sapiens LST1 mRNA, C1ST1 splice variant, complete cds. /FEA=mRNA /GEN=LST1 /DB_XREF=gi:2145065 /UG=Hs.88111 lymphocyte antigen 117 /FL=gb:AE000425.1
205329_s_at	gb:NM_0037194.1 /DEF=Homo sapiens sorting nexin 4 (SNX4) mRNA. /FEA=mRNA /GEN=SNX4 /PROD=sorting nexin 4 /DB_XREF=gi:1507144 /UG=Hs.267812 sorting nexin 4 /FL=gb:AE130078.1 qb:NM_0037194.1
218194_at	gb:NM_015523.1 /DEF=Homo sapiens small fragment nuclelease (DKFZP066E144) mRNA. /FEA=mRNA /GEN=DKFZP066E144 /PROD=small fragment nuclelease /DB_XREF=gi:17661615 /UG=Hs.7527 small fragment nuclelease /FL=gb:AE154872.1 qb:AL110239.1 qb:NM_015523.1
220560_at	gb:NM_014144.1 /DEF=Homo sapiens SN53 protein (SMS3) mRNA. /FEA=mRNA /GEN=SMS3 /PROD=SMS3 protein /DB_XREF=gi:7662662 /UG=Hs.272100 SMS3 protein /FL=gb:AB0239486.1 qb:NM_014144.1
208270_s_at	gb:NM_020216.2 /DEF=Homo sapiens arginyl aminopeptidase (aminopeptidase B) (RNPEP) mRNA. /FEA=mRNA /GEN=RNPEP /PROD=arginyl aminopeptidase (aminopeptidase B) /DB_XREF=gi:13443030 /UG=Hs.283667 arginyl aminopeptidase (aminopeptidase B) /FL=gb:NM_020216.2
220175_s_at	gb:NM_020667.1 /DEF=Homo sapiens hypothetical protein from clone 1659351 (LOC57397) mRNA. /FEA=mRNA /GEN=LOC57397 /PROD=hypothetical protein from clone 1659351 /FL=gb:NM_020667.1
212429_s_at	Consensus includes gb:AW194657 /FEA=EST /DB_XREF=gi:64173537 /DB_XREF=est:xb28512.x1 /CLONE=IMAGE:2577199 /UG=Hs.75782 general transcription factor IIIc, polypeptide 2 (beta subunit, 110kd)

209058_at	gb:AB002282.1 /DEF=Homo sapiens mRNA for NMBF1alpha, complete cds. /FEA=mRNA /PROD=hnBFLalpha /DB_XREF=gi:6526354 /UG=Hs.174050 endothelial differentiation-related factor 1 /FL=gb:NM_003792.1 gb:AB002282.1
212535_at	Consensus includes gb:AA142929 /FEA=EST /DB_XREF=est:2140207.s1 /CLONE=IMAGE:504444 /UG=Hs.288993 ESTs
201524_x_at	gb:NM_003318.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) (UBE2N), mRNA. /FEA=mRNA /GEN=UBE2N /PROD=ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) /FL=gb:D83004.1 gb:BC00396.1 gb:NM_003348.1
201716_at	gb:NM_003099.1 /DEF=Homo sapiens sorting nexin 1 (SNX1), mRNA. /FEA=mRNA /GEN=SNX1 /PROD=sorting nexin 1 /DB_XREF=gi:14507138 /UG=Hs.75283
213097_s_at	Consensus includes gb:AA1338837 /FEA=EST /DB_XREF=est:1928509.x1 /CLONE=IMAGE:1933665 /UG=Hs.82254 zuotin related factor 1
213532_at	Consensus includes gb:AA1797833 /FEA=EST /DB_XREF=gi:5363390 /DB_XREF=est:1979810.x1 /CLONE=IMAGE:2386986 /UG=Hs.52438 ESTs, Weakly similar to ORF YOR126c S.cerevisiae
210766_s_at	gb:AE033640.1 /DEF=Homo sapiens trachea cellular apoptosis susceptibility protein /DB_XREF=gi:3560554 /UG=Hs.90073 chromosome segregation 1 (yeast homolog)-like /FL=gb:AF053640.1
209523_at	Consensus includes gb:AK001618.1 /DEF=Homo sapiens cDNA FLJ10756 Fis, clone NT2RP2004572, highly similar to Homo sapiens cofactor of initiator function mRNA. /FEA=mRNA /DB_XREF=gi:1022983 /UG=Hs.122752 TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150KD /FL=gb:AF02645.1 gb:AF040701.1 gb:AF057694.1 gb:NM_003584.1
209276_s_at	gb:AF162769.1 /DEF=Homo sapiens thioltransferase mRNA, complete cds. /FEA=mRNA /PROD=thioltransferase /DB_XREF=gi:542445 /UG=Hs.28988 glutaredoxin (thioltransferase) /FL=gb:BC005304.1 gb:AF162769.1 gb:D21238.1
200848_at	Consensus includes gb:AA479488 /FEA=EST /DB_XREF=gi:220804 /DB_XREF=est:zv21c09.s1 /CLONE=IMAGE:754288 /UG=Hs.4113 S-adenosylhomocysteine hydrolase-like 1 /FL=gb:UB2761.1 /FEA=mRNA /gb:NM_005621.1
212406_s_at	Consensus includes gb:AB028973.1 /DEF=Homo sapiens mRNA for KIAA1050 protein, partial cds. /FEA=mRNA /GEN=KIAA1050 /PROD=KIAA1050 protein /DB_XREF=gi:15689436 /UG=Hs.184628 hypothetical protein FLJ10883
212072_s_at	Consensus includes gb:AA109761 /DEF=Human DNA sequence from clone RP5-863C7 on chromosome 20p12.3-13. Contains the CSNK2A1 gene for casein kinase 2 alpha 1 polypeptide (EC 2.7.1.37), ESTs, STSs and GSSs /FEA=mRNA /DB_XREF=gi:5738437 /UG=Hs.155140 casein kinase 2, alpha 1 polypeptide
203159_at	gb:NM_014905.1 /DEF=Homo sapiens glutaminase (GLS), mRNA. /FEA=mRNA /GEN=GLS /PROD=glutaminase C /DB_XREF=gi:7662327 /UG=Hs.239189 glutamine /FL=gb:AF227434.1 gb:AB020645.1 gb:AB097493.1 gb:AF223913.1 qb:RN_014905.1
203521_s_at	gb:NM_014315.1 /DEF=Homo sapiens endocrine regulator (HRHFB2), mRNA. /FEA=mRNA /GEN=HRHFB2136 /PROD=endocrine regulator /DB_XREF=gi:7657183 /UG=Hs.48433 endocrine regulator /FL=gb:AF121141.1 qb:NM_014345.1
204439_at	gb:NM_006820.1 /DEF=Homo sapiens hypothetical protein, expressed in osteoblast (SS3666), mRNA. /FEA=mRNA /GEN=SS3666 /PROD=hypothetical protein, expressed in osteoblast /DB_XREF=gi:11006526 /DB_XREF=est:AU145005 /CLONE=HEMRA1003603 /UG=Hs.44450 Sp3 transcription
210371_s_at	gb:NM_006820.1 /DEF=Homo sapiens hypothetical protein 4, clone MG:1393, mRNA, complete cds. /FEA=mRNA /PROD=Similar to retinoblastoma binding protein 4 /FL=gb:BC003092.1 qb:NM_005610.1
200052_s_at	gb:NM_004515.1 /DEF=Homo sapiens interleukin enhancer binding factor 2, 45kD (ILF2), mRNA. /FEA=mRNA /GEN=ILF2 /PROD=interleukin enhancer binding factor 2, 45kD /FL=gb:BC000382.1 qb:NM_004515.1
201019_s_at	gb:NM_001112.1 /DEF=Homo sapiens eukaryotic translation initiation factor 1A (EFLA), mRNA. /FEA=mRNA /GEN=EFLA /PROD=eukaryotic translation initiation factor 1A /DB_XREF=gi:4503498 /UG=Hs.4310 eukaryotic translation initiation factor 1A /FL=gb:BC000793.1 qb:118900.1
219892_at	gb:NM_023003.1 /DEF=Homo sapiens transmembrane 6 superfamily member 1 (TM6SF1), mRNA. /FEA=mRNA /GEN=TM6SF1 /PROD=transmembrane 6 superfamily member 1 /DB_XREF=gi:1319198 /UG=Hs.133805 transmembrane 6 superfamily member 1 /FL=gb:PF255922.1 qb:NM_023003.1
218095_s_at	gb:NM_018475.1 /DEF=Homo sapiens uncharacterized hypothalamus protein HMP (LOC55858), mRNA. /FEA=mRNA /GEN=LOC55858 /PROD=uncharacterized hypothalamus protein HMP /DB_XREF=gi:8923860 /UG=Hs.23651 uncharacterized hypothalamus protein HMP /FL=gb:BC003545.1 qb:AF220188.1

218042_at	gb:Nm_016129.1 /DEF=Homo sapiens COP9 complex subunit 4 (LOC51138), mRNA. /FEA=mRNA /GEN=LOC51138 /PROD=COP9 complex subunit 4
202172_at	/DB_XREF=gi:705644 /UG=Hs.6671 COP9 complex subunit 4 /FI=gb:BC004302.1 /gb:AF100757.1 qb:NM_016129.1
218108_at	Consensus includes gb:BG035116 /FEA=EST /DB_XREF=gi:12428927 /DB_XREF=est:602324811F1 /CLONE=IMAGE:4412907 /UG=Hs.6557 zinc finger protein 161 /FL=gb:D28118.1 qb:Nm_0071146.1
218108_at	gb:Nm_018108.1 /DEF=Homo sapiens hypothetical protein FLJ10483 (FLJ10483), mRNA. /FEA=mRNA /GEN=FLJ10483 /PROD=hypothetical protein
212539_at	FLJ10483 /DB_XREF=gi:118922451 /UG=Hs.6877 hypothetical protein FLJ10483 /FI=gb:NM_018108.1
212539_at	Consensus includes gb:AI422099 /FEA=EST /DB_XREF=gi:14268030 /DB_XREF=est:t257h09.x1 /CLONE=IMAGE:21030425 /UG=Hs.14570 hypothetical protein FLJ22530
212635_at	Consensus includes gb:AN161626 /FEA=EST /DB_XREF=gi:116300659 /DB_XREF=est:au68b11.x1 /CLONE=IMAGE:2781405 /UG=Hs.21739 Homo sapiens mRNA; cDNA DKEFp58G11518 (from clone DKFZp58G11518)
203356_at	Consensus includes gb:BB349584 /FEA=EST /DB_XREF=gi:19261437 /DB_XREF=est:ht55h12.x1 /CLONE=IMAGE:3150695 /UG=Hs.7145 calpain 7 /FL=gb:AB028539.1 qb:Nm_014296.1
208174_x_at	gb:Nm_005089.1 /DEF=Homo sapiens U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2 /FI=gb:D49677.1 qb:NM_005089.1
53912_at	PROD=U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2 /FI=gb:D49677.1 qb:NM_005089.1
Cluster Incl. AI668643:zb13f10.x5 Homo sapiens cDNA, 3' end /clone=IMAGE-301963 /clone_end-3 /gb:AI668643 /gi:4827951 /ug=Hs.15827 /len=601	
221736_at	Consensus includes gb:AN156777 /FEA=EST /DB_XREF=est:z118c08.s1 /CLONE=IMAGE:502286 /UG=Hs.25431 KIAA1219 protein
209475_at	gb:AF106069.1 /DEF=Homo sapiens deubiquitinating enzyme (UNP04) mRNA, complete cds. /FEA=mRNA /GEN=UNP04 /PROD=deubiquitinating enzyme /DB_XREF=gi:1:5814096 /UG=Hs.2316B ubiquitin specific protease 15 /FI=gb:AF03990.1 qb:AF106069.1
204366_s_at	gb:NM_001521.1 /DEF=Homo sapiens general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD) (GTfE3G2), mRNA. /FEA=mRNA /GEN=GTF3C2 /PROD=general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD) /FI=gb:DI3636.1 qb:NM_001521.1 /DB_XREF=gi:4504204 /UG=Hs.75782 general transcript, polypeptide factor IIIC, polypeptide 2 (beta subunit, 110kD) /FI=gb:DI3636.1 qb:NM_001521.1
212584_at	Consensus includes gb:BG260519 /FEA=EST /DB_XREF=gi:12770335 /DB_XREF=est:602372055F1 /CLONE=IMAGE:4460024 /UG=Hs.129952 KIAA0560 gene product
212140_at	Consensus includes gb:AB014548.1 /DEF=Homo sapiens mRNA for KIAA0648 protein /FI=gb:NM_0172109 /UG=Hs.31921 KIAA0648 protein /DB_XREF=gi:3327109 /UG=Hs.31921 KIAA0648 protein
219083_at	gb:Nm_018130.1 /DEF=Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. /FEA=mRNA /GEN=FLJ10539 /PROD=hypothetical protein FLJ10539 /FI=gb:NM_018130.1
215772_x_at	Consensus includes gb:AI40226.1 /DEF=Homo sapiens mRNA; cDNA DKFZp58G6M2023 (from clone DKFZp58G6M2023); partial cds. /FEA=mRNA /GEN=DKFZp58G6M2023 /PROD=hypothetical protein /DB_XREF=gi:1:881469 /UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit
216194_s_at	Consensus includes gb:AD001527 /DEF=Homo sapiens DNA from chromosome 19-cosmid f24590 containing CAPNS and P0L2R1, genomic sequence /FEA=CDS
204373_s_at	gb:Nm_014610.1 /DEF=Homo sapiens cytoskeleton-associated protein 1 (KIAA0480), mRNA. /FEA=mRNA /GEN=KIAA0480 /PROD=KIAA0480 gene product /DB_XREF=gi:1:1905899 /UG=Hs.31053 cytoskeleton-associated protein 1
208927_at	gb:NM_019615.1 /DEF=Homo sapiens KIAA0480 gene product /FI=gb:AB007949.1 qb:NM_014810.1 /DB_XREF=gi:111947783 /DB_XREF=est:602137554F1 /CLONE=IMAGE:4274077 /UG=Hs.129951 speckle-type P02 protein /FI=gb:BC001269.1
220146_at	gb:Nm_016562.1 /DEF=Homo sapiens toll-like receptor 7 (LOC51284), mRNA. /FEA=mRNA /GEN=LOC51284 /PROD=toll-like receptor 7 /DB_XREF=gi:1:7706092 /UG=Hs.179152 toll-like receptor 7 /FI=gb:AE240467.1 qb:NM_016562.1
219694_at	gb:Nm_019018.1 /DEF=Homo sapiens hypothetical protein (FLJ11127), mRNA. /FEA=mRNA /GEN=FLJ11127 /PROD=hypothetical protein /DB_XREF=gi:95066640 /UG=Hs.91165 hypothetical protein /FI=gb:NM_019018.1
213229_at	Consensus includes gb:BF590131 /FEA=EST /DB_XREF=est:nab19e04.x1 /CLONE=IMAGE:3266383 /UG=Hs.87889 helicase-mot
214356_s_at	Consensus includes gb:AI272899 /FEA=EST /DB_XREF=est:q141c07.x1 /CLONE=IMAGE:18715468 /UG=Hs.3852 KIAA0368 protein
213153_at	Consensus includes gb:AB02899.1 /DEF=Homo sapiens mRNA for KIAA076 protein, partial cds. /FEA=mRNA /GEN=KIAA076 /PROD=KIAA076 protein /DB_XREF=gi:1:5689488 /UG=Hs.154525 KIAA076 protein
218294_s_at	gb:AF267855.1 /DEF=Homo sapiens DC41 mRNA, complete cds. /FEA=mRNA /GEN=DC41 /DB_XREF=gi:12006056 /UG=Hs.271623 nucleoporin 50kD /FI=gb:AF267855.1 qb:NM_007172.1 qb:AF16624.1
221522_at	gb:AL36714.1 /DEF=Homo sapiens mRNA; cDNA DKFZp134I0718 (from clone DKFZp134I0718); complete cds. /FEA=mRNA /GEN=DKFZp434I0718 /PROD=hypothetical

	protein /DB_XREF=gi:12053080 /UG-Hs.59236 Homo sapiens mRNA; cDNA DK57p434I0718 (from clone DKF2p434I0718); complete cds /FL=gb:NM_136784.1
205930_at	gb:NM_005513.1 /DEF=Homo sapiens general transcription factor IIIE, polypeptide 1 (alpha subunit, 56kd) (GTF2E1), mRNA. /FEA=mRNA
	PROD=general transcription factor IIIE, polypeptide 1 (alpha subunit, 56kd) /DB_XREF=gi:5031726 /UG-Hs.145381 general transcription factor IIIE, polypeptide 1 (alpha subunit, 56kd) /FL=gb:NM_005513.1
210312_s_at	gb:BC002640.1 /DEF=Homo sapiens, similar to uterine protein, clone MGC:4279, mRNA, complete cds. /FEA=mRNA /PROD=Similar to uterine protein /DB_XREF=gi:120803610 /UG-Hs..1187 hypothetical protein 24636 /FL=gb:BC002640.1
213838_at	Consensus includes gb:DA191426 /FEA=EST /DB_XREF=est:ap83909.s1 /CLONE=IMAGE:626848 /UG-Hs.279886 RAN binding protein 9
202520_s_at	gb:NM_000249.1 /DEF=Homo sapiens mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2) (MLH1), mRNA. /FEA=mRNA /GEN=MLH1 /PROD=mutL homolog 1 /DB_XREF=gi:4557756 /UG-Hs.57301 mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2) /FL=gb:NM_000249.1 gb:U07343.1
221834_at	Consensus includes gb:AV700132 /FEA=EST /DB_XREF=est:AV700132 /CLONE:GRGS03 /UG-Hs.295923 seven in absentia (Drosophila) homolog 1
210942_s_at	gb:AB022918.1 /DEF=Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds. /FEA=mRNA /GEN=ST3Gal VI /PROD=alpha2,3-sialyltransferase ST3Gal VI /DB_XREF=gi:4827246 /UG-Hs.34578 alpha2,3-sialyltransferase /FL=gb:AB022918.1
202396_at	gb:NM_006706.1 /DEF=Homo sapiens transcription factor CA150 (CA150), mRNA. /FEA=mRNA /GEN=CA150 /PROD=transcription factor CA150
219598_s_at	gb:NM_0729753 /UG-Hs.13063 transcription factor CA150 /FL=gb:AF017789.1 gb:NM_006706.1
202502_at	gb:NM_00016.1 /DEF=Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACADM /PROD=acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain proenzyme /DB_XREF=gi:4557230
211958_s_at	gb:NM_014175.1 /DEF=Homo sapiens HSPC145 protein (HSPC145), mRNA. /GEN=HSPC145 /PROD=HSPC145 protein /DB_XREF=gi:7661605 /UG-Hs.19158 acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain /FL=gb:BC005317.1 gb:NM_000016.1 gb:AF251043.1
218027_at	gb:NM_014175.1 /DEF=Homo sapiens sorting nexin 5 (SNX5), mRNA. /FEA=mRNA /GEN=SNX5 /PROD=sorting nexin 5 /DB_XREF=gi:7657598 /UG-Hs.13794
217792_at	gb:NM_01426.1 /DEF=Homo sapiens sorting nexin 5 (SNX5), mRNA. /FEA=mRNA /GEN=SNX5 /PROD=sorting nexin 5 /DB_XREF=gi:7657598 /UG-Hs.13794
221036_s_at	gb:NM_03101.1 /DEF=Homo sapiens hypothetical protein DK2p56D0372 (DK2p56D0372), mRNA. /FEA=mRNA /GEN=DKEZB564D0372 /PROD=DKEZB564D0372
201723_s_at	gb:U41514.1 /DEF=Human UDP-GalNAc polypeptide N-acetylgalactosaminyltransferase mRNA, complete cds. /FEA=mRNA /PROD=UDP-GalNAc-polypeptidN-acetylgalactosaminyltransferase /DB_XREF=gi:1.1.3.284 /UG-Hs.80120 UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) 7FL=gb:U41514.1 gb:NM_020474.2
202351_at	Consensus includes gb:AI03579 /FEA=EST /DB_XREF=est:AI03579 /DB_XREF=est:432555 /DB_XREF=est:432555.x1 /CLONE=IMAGE:1696378 /UG-Hs.295726 integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) /FL=gb:NM_002210.1
208833_s_at	gb:U118887.1 /DEF=Human calnexin mRNA, complete cds. /FEA=mRNA /PROD=calnexin /DB_XREF=gi:306480 /UG-Hs.155560 calnexin /FL=gb:NM_001746.1
213278_at	Consensus includes gb:AW014788 /FEA=EST /DB_XREF=gi:5863545 /DB_XREF=est:U1-H-B10-aes-h-10-0-U1.s1 /CLONE=IMAGE:2709354 /UG-Hs.18802 Homo sapiens clone 23632 mRNA sequence
203447_at	Consensus includes gb:AU157008 /FEA=EST /DB_XREF=est:AU157008 /CLONE=PLACE:005711 /UG-Hs.193725 proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 /FL=gb:NM_005047.1
212459_x_at	Consensus includes gb:BF53940 /FEA=EST /DB_XREF=est:1.1.686264 /DB_XREF=est:nab48F10.x1 /CLONE=IMAGE:3269154 /UG-Hs.247309 succinate-CoA ligase, GTP-forming, beta subunit
218514_at	gb:NM_018149.1 /DEF=Homo sapiens hypothetical protein FLJ10587 (FLJ10587), mRNA. /FEA=mRNA /GEN=FLJ10587 /PROD=hypothetical protein FLJ10587 /DB_XREF=gi:8922339 /UG-Hs.7296 hypothetical protein FLJ10587 /FL=gb:NM_018149.1
212648_at	Consensus includes gb:AL079292.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROTIMAGE 48814. /FEA=mRNA /PROD=hypothetical protein, similar to (AC007017) putative RNA helicase A Arabidopsis thaliana /DB_XREF=gi:1.5102732 /UG-Hs.95665 hypothetical protein
200708_at	gb:NM_002080.1 /DEF=Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=GOT2 /PROD=aspartate aminotransferase 2 precursor /DB_XREF=gi:4504068 /UG-Hs.170197 glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) /FL=gb:BC000525.1 gb:NM_002080.1

201064_s_at	gb:NM_003819.2 /DEF=Homo sapiens poly(A)-binding protein, cytoplasmic 4 (inducible form) /DB_XREF=gi:6552335 /UG-Hs.169900 poly(A)-binding protein, cytoplasmic 4 (inducible form) /FEA=mRNA /GEN=PABC4
218604_at	gb:NM_014319.2 /DEF=Homo sapiens integral inner nuclear membrane protein (MAN1), mRNA. /FEA=mRNA /GEN=MAN1 /PROD=Integral inner nuclear membrane protein /FL=gb:AF112299.2 /gb:NM_014319.2
214864_s_at	Consensus includes gb:AK0243861 /DB_XREF=gi:7706606 /UG=Hs.7256 Integral inner nuclear membrane protein /FEA=mRNA /GEN=CDC16 /PROD=CDC16
202717_s_at	gb:NM_003903.1 /DEF=Homo sapiens cDNA FLJ13124 fis, clone PIAC54000100, highly similar to Homo sapiens hydroxypyruvate reductase (GRHPR) gene. /FEA=mRNA /GEN=CDC16 /PROD=CDC16
201643_x_at	gb:NM_003903.1 /DEF=Homo sapiens CDC16 (cell division cycle 16, S cerevisiae, homolog) /DB_XREF=gi:14502700 /UG=Hs.1592 CDC16 (cell division cycle 16, S. cerevisiae, homolog) /
213803_at	gb:NM_016604.1 /DEF=Homo sapiens LOC51780 /DB_XREF=gi:7706598 /UG=Hs.24125 putative zinc finger protein /FL=gb:AF251039.1 /mRNA. /FEA=mRNA /GEN=LOC51780 /PROD=putative zinc finger protein
204689_at	Consensus includes gb:RG545463 /FEA=EST /DB_XREF=est:60257265f1 /CLONE=IMAGE:4701118 /UG=Hs.180446 karyopherin (importin) beta 1
218228_s_at	gb:NM_001529.1 /DEF=Homo sapiens hematopoietically expressed homeobox (HHEX), mRNA. /FEA=mRNA /GEN=RHEX /PROD=hematopoietically expressed homeobox /FL=gb:NM_001529.1 /gb:gb:NM_002729.1
202918_s_at	gb:NM_025335.1 /DEF=Homo sapiens tankyrase 2 (TNKL), mRNA. /FEA=mRNA /GEN=TNKL /PROD=tankyrase 2 /DB_XREF=gi:13376841 /UG=Hs.280776 tankyrase 2 /FL=gb:AF264912.1 /gb:AF329882.1
212263_at	gb:AF11853.1 /DEF=Homo sapiens CG1-95 protein mRNA, complete cds. /FEA=mRNA /PROD=CG1-95 protein /DB_XREF=gi:4929658 /UG=Hs.107942 DKFZP54M412 protein /FL=gb:AB015441.1 /gb:BC005237.1 /gb:AF11853.1 /gb:AL080010.1 /gb:NM_015387.1
221825_at	Consensus includes gb:AF1114716 /FEA=EST /DB_XREF=gi:6360061 /DB_XREF=est:HAL315 /UG=Hs.150200 homolog of mouse quaking QKI (KH domain RNA binding protein) /FL=gb:AF142419.1 /gb:AF14422.1
211047_x_at	Consensus includes gb:AU151793 /FEA=EST /DB_XREF=est:AU151793 /CLONE=NT2RP2006115 /UG=Hs.157078 Homo sapiens cDNA FLJ12193 fis, clone NT2RP2002033
209798_at	gb:BC006331.1 /DEF=Homo sapiens, clone MGC:12798, mRNA, complete cds. /FEA=mRNA /GEN=NPAT /DB_XREF=gi:1304113 /UG=Hs.89385 nuclear protein, ataxia-telangiectasia locus /FL=gb:BC006331.1
204361_s_at	gb:AB014406.1 /DEF=Homo sapiens mRNA for RA70, complete cds. /FEA=mRNA /GEN=RA70 /PROD=RA70 /DB_XREF=gi:14062959 /UG=Hs.52644 SKP55 homolog /FL=gb:BC002893.1 /gb:AF072116.1 /gb:AB014406.1 /gb:AF051323.1 /gb:NM_002519.1
218127_at	Consensus includes gb:AF1804118 /FEA=EST /DB_XREF=gi:5369890 /DB_XREF=est:tc68e01.x1 /CLONE=IMAGE:2069784 /UG=Hs.84928 nuclear transcription factor Y, /FL=gb:NM_006166.2 /gb:BC005316.1 /gb:BC005317.1 /gb:LO6145.1
220355_s_at	gb:NM_018165.1 /DEF=Homo sapiens hypothetical protein FLJ10645 (FLJ10645), mRNA. /FEA=mRNA /GEN=FLJ10645 /PROD=hypothetical protein FLJ10645 /DB_XREF=gi:8922564 /UG-Hs.14143 polybromo 1 /FL=gb:AF117387.1 /gb:NM_018165.1
202930_s_at	gb:NM_003650.1 /DEF=Homo sapiens succinate-coA ligase, ADP-forming, beta subunit /DB_XREF=gi:111321562 /UG=Hs.182217 succinate-coA ligase, ADP-forming, beta subunit /FL=gb:NM_003650.1
203745_at	Consensus includes gb:AF1801013 /FEA=EST /DB_XREF=gi:53666485 /DB_XREF=est:wg15d09.x1 /CLONE=IMAGE:2355169 /UG=Hs.211571 holocytocchrome c synthase (cytochrome c heme-lyase) /FL=gb:U36787.1 /gb:NM_005333.1
200597_at	Consensus includes gb:AF123230 /FEA=EST /DB_XREF=est:qab810.x1 /CLONE=IMAGE:1689978 /UG=Hs.198899 eukaryotic translation initiation factor 3, subunit 3, (theta, 150170kb) /FL=gb:DO0929.1 /gb:US8046.1 /gb:U78311.1 /gb:NM_003750.1
218519_at	gb:NM_011945.1 /DEF=Homo sapiens hypothetical protein FLJ20730 (FLJ20730), mRNA. /FEA=mRNA /GEN=FLJ20730 /PROD=hypothetical protein FLJ20730 /DB_XREF=gi:8923656 /UG-Hs.237480 hypothetical protein
203947_at	gb:NM_001326.1 /DEF=Homo sapiens cleavage stimulation factor, 3 pre-RNA, subunit 3, 77kD (CSF3), mRNA. /FEA=mRNA /GEN=CSF3 /PROD=cleavage stimulation factor subunit 3 /DB_XREF=gi:4557494 /UG-Hs.18034 cleavage stimulation factor, 3 pre-RNA, subunit 3, 77kD /FL=gb:NM_001326.1 /gb:U15782.1
219002_at	gb:NM_024622.1 /DEF=Homo sapiens hypothetical protein FLJ21901 (FLJ21901), mRNA. /FEA=mRNA /GEN=FLJ21901 /PROD=hypothetical protein FLJ21901 /DB_XREF=gi:13315843 /UG=Hs.32646 hypothetical protein FLJ21901 /FL=gb:NM_024622.1
220122_at	gb:NM_024117.1 /DEF=Homo sapiens hypothetical protein FLJ22344 (FLJ22344), mRNA. /FEA=mRNA /GEN=FLJ22344 /PROD=hypothetical protein FLJ22344 /DB_XREF=gi:13316020 /UG=Hs.10716 hypothetical protein FLJ22344 /FL=gb:NM_024717.1
203882_at	gb:NM_005684.1 /DEF=Homo sapiens interferon-stimulated transcription factor 3, gamma (48kd) (ISGF3G), mRNA. /FEA=mRNA /GEN=ISGF3G /PROD=interferon-stimulated transcription factor 3, gamma (48kd) /DB_XREF=gi:1517474 /UG=Hs.1706 interferon-stimulated transcription factor

3, gamma (48kd) /FI=gb:M87503.1 gb:NM_006084.1	
Consensus includes gb:W02312 /FEA=EST /DB_XREF=gi:11214291 /DB_XREF=est:za08d08_r1 /CLONE_IMAGE:291951 /UG-Hs_171911 adenylylate kinase 2	
gb:NM_004175.1 /DEF=Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kd) (SNRPD3) mRNA, /GEN=SNRPD3 /PROD=small nuclear ribonucleoprotein D3 polypeptide (18kd) /FI=gb:BC000457.1 gb:NM_004175.1 gb:U15009.1	
gb:NM_020202.1 /DEF=Homo sapiens Nif protein 2 (NIT2), mRNA, /FEA=mRNA /GEN=NIT2 /PROD=Nif protein 2 /DB_XREF=gi:19910459 /UG-Hs_15627 Nit protein 2 /FI=gb:AF260334.1 gb:AF284574.1 gb:NM_020202.1	
Consensus includes gb:AK026168.1 /DEF=Homo sapiens cDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 mRNA sequence. /FEA=mRNA /DB_XREF=gi:10438931 /UG-Hs_188882 Homo sapiens cDNA: FLJ21862 fis, clone HSP02321, highly similar to AF052101 Homo sapiens clone 23872 mRNA sequence	
201990_s_at gb:NM_001310.1 /DEF=Homo sapiens cAMP responsive element binding protein-like 2 (CREB2), mRNA, /FEA=mRNA /GEN=CREB2 /PROD=cAMP responsive element binding protein-like 2 /FI=gb:AF030801.1	
gb:NM_001310.1 /DEF=Human deoxyuridine triphosphatase (DUT) mRNA, complete cds. /FEA=mRNA /GEN=DUT /PROD=deoxyuridine triphosphatase /DB_XREF=gi:1121817 /UG-Hs_82113 dUTP pyrophosphatase /FI=gb:AB019113.1 qb:US1930.1 qb:U2891.1 qb:U2891.1 qb:NM_001948.1	
Consensus includes gb:AI171641 /FEA=EST /DB_XREF=gi:5545690 /DB_XREF=est:we28104.x1 /CLONE=IMAGE:2342431 /UG-Hs_306623 Homo sapiens cDNA FLJ1202 fis, clone HMBB1001668	
201198_s_at Consensus includes gb:AI860431 /FEA=EST /DB_XREF=gi:55114047 /DB_XREF=est:w113h07.x1 /CLONE=IMAGE:2424829 /UG-Hs_3887 proteasome (prosome, macrophain) 26S subunit, non-ATPase, 1 /FI=gb:D44166.1 qb:NM_002607.1	
203010_at gb:NM_003152.1 /DEF=Homo sapiens signal transducer and activator of transcription 5A (STAT5A), mRNA, /FEA=mRNA /GEN=STAT5A /PROD=signal transducer and activator of transcription 5A /DB_XREF=gi:4507256 /UG-Hs_167503 signal transducer and activator of transcription 5A /FI=gb:U43185.1 qb:NM_003152.1 qb:U141142.1	
218067_s_at gb:NM_018011.1 /DEF=Homo sapiens hypothetical protein FLJ10154 (FLJ10154), mRNA, /FEA=mRNA /GEN=FLJ10154 /PROD=hypothetical protein FLJ10154 /DB_XREF=gi:1799712 hypothetical protein FLJ10154 /FI=gb:NM_018011.1	
219077_s_at gb:NM_016373.1 /DEF=Homo sapiens WW domain-containing oxidoreductase (WWOX), mRNA, /FEA=mRNA /GEN=WWOX /PROD=FOR II /DB_XREF=gi:17706522 /UG-Hs_519 WW domain-containing oxidoreductase /FI=gb:AF211943.1 qb:NM_016373.1 qb:AF227527.1	
215424_s_at Consensus includes gb:AV689564 /FEA=EST /DB_XREF=est:AV7689564 /CLONE=GRCEA06 /UG-Hs_79008 SKI-INTERACTING PROTEIN precursor /DB_XREF=gi:10291427 /DB_XREF=est:AV7689564 /CLONE=GRCEA06 /UG-Hs_79008 SKI-INTERACTING PROTEIN	
219043_s_at gb:NM_024665.1 /DEF=Homo sapiens hypothetical protein MGC3062 (MGC3062), mRNA, /FEA=mRNA /GEN=MGC3062 /PROD=hypothetical protein MGC3062 /DB_XREF=gi:13129043 /UG-Hs_90576 hypothetical protein MGC3062 /FI=gb:AE671853.1 qb:BC001021.1 qb:NM_024065.1	
209313_at gb:AB044661.1 /DEF=Homo sapiens XPA binding protein 1, complete cds. /FEA=mRNA /GEN=XAP1 /PROD=XPA binding protein 1 /DB_XREF=gi:11:01094140 /UG-Hs_18259 XPA binding protein 1; putative ATP (GTP)-binding protein /FI=gb:AB044661.1	
202944_at gb:NM_00062.1 /DEF=Homo sapiens N-acetylglactosaminidase, alpha- (NAGA), mRNA, /FEA=mRNA /GEN=NAGA /PROD=alpha-N-acetylglactosaminidase precursor /DB_XREF=gi:4557780 /UG-Hs_75372 N-acetylglactosaminidase, alpha- /FI=gb:BC000095.1 qb:NM_038033.1 qb:NM_000262.1	
/FEA=mRNA /PROD=eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kd) /DB_XREF=gi:16650833 /UG-Hs_83126 TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kd /FI=gb:D63705.1 qb:NM_005643.1 qb:AF118094.1	
211656_x_at gb:NM_003676.1 /DEF=Homo sapiens degenerative spermatocyte (homolog Drosophila; lipid desaturase) (DEGS), mRNA, /FEA=mRNA /GEN=DEGS /PROD=degenerative spermatocyte /DB_XREF=gi:4505192 /UG-Hs_185973 degenerative spermatocyte (homolog Drosophila; lipid desaturase) /FI=gb:AF02668.1 qb:NM_003676.1	
213070_at Consensus includes gb:AV682436 /FEA=EST /DB_XREF=gi:110284299 /DB_XREF=est:AV682436 /CLONE=SKRBB008 /UG-Hs_5848 Homo sapiens mRNA, cDNA DKF25564122 (from clone DKF25564122)	
201111_at gb:AF036364.1 /DEF=Homo sapiens brain cellular apoptosis susceptibility protein (CSE1) mRNA, complete cds. /FEA=mRNA /GEN=CSE1 /PROD=cellular apoptosis susceptibility protein /DB_XREF=gi:3560556 /UG-Hs_90073 chromosome segregation 1 (yeast homolog)-like /FI=gb:U133286.1 qb:AF053641.1 qb:NM_001316.1	
204370_at gb:NM_006831.1 /DEF=Homo sapiens ATPGTP-binding protein (HSPAB), mRNA, /FEA=mRNA /GEN=HSPAB /PROD=ATPGTP-binding protein /FI=gb:BC000446.1 qb:U73524.1 qb:NM_006831.1 /UG-Hs_87465 ATPGTP-binding protein /FI=gb:BC000446.1 qb:U73524.1 qb:NM_006831.1	

202911_at	gb:NM_000119.1 /DEF=Homo sapiens mutS (E. coli) homolog 6 (MSH6) , mRNA. /FEA=mRNA /GEN=MSH6 /PROD=muts (E. coli) homolog 6 /DB_XREF=gi:4504190 /UG=Hs.3248 mutS (E. coli) homolog 6 /FL=gb:U28946..1 qb:NM_000119.1 qb:U54771.2
204197_s_at	gb:NM_004350.1 /DEF=Homo sapiens runt-related transcription factor 3 (RUNX3) , mRNA. /FEA=mRNA /GEN=RUNX3 /PROD=runt-related transcription factor 3 /DB_XREF=gi:1757917 /UG=Hs.170019 runt-related transcription factor 3 /FL=gb:NM_004350.1
217809_at	gb:NM_014038.1 /DEF=Homo sapiens HSPC028 protein (HSPC028) , mRNA. /FEA=mRNA /GEN=HSPC028 /PROD=HSPC028 protein /DB_XREF=gi:7661743 /UG=Hs.5216 HSPC028 protein /FL=gb:AF083246..1 qb:NM_014038.1
201054_at	Consensus includes qb:SE966599 /FEA=EST /DB_XREF=gi:1172191 /DB_XREF=est:601660283R1 /CLONE_IMAGE:3906044 /UG=Hs.77492 heterogeneous nuclear ribonucleoprotein A0 /FL=gb:BC001008..1 qb:NM_006805.1 qb:U23803..1
200994_at	Consensus includes qb:SE966599 /FEA=EST /DB_XREF=est:602386007F1 /CLONE_IMAGE:4515240 /UG=Hs.5151 RAN binding protein 7 /FL=gb:AF098799..1 qb:NM_006391.1
201572_x_at	gb:NM_0011921.1 /DEF=Homo sapiens deaminase (DCTD) , mRNA. /FEA=mRNA /GEN=DCTD /PROD=dCMP deaminase /DB_XREF=gi:4503276 /UG=Hs.76894 dCMP deaminase /FL=gb:L12136..1 qb:NM_0011921.1
218195_at	gb:NM_024573.1 /DEF=Homo sapiens hypothetical protein FLJ12910 , mRNA. /FEA=mRNA /GEN=FLJ12910 /PROD=hypothetical protein FLJ12910 /
219905_at	DB_XREF=gi:13375745 /UG=Hs.15929 hypothetical protein FLJ12910 /FL=gb:NM_024573..1
203932_at	gb:NM_018538.1 /DEF=Homo sapiens hypothetical protein PRO2801 , mRNA. /FEA=mRNA /GEN=PRO2801 /PROD=hypothetical protein PRO2801 /DB_XREF=gi:8924201 /UG=Hs.181223 hypothetical protein PRO2801 /FL=gb:AF11.9899..1 qb:NM_018538..1 Consensus includes qb:AF168580 /FEA=EST /DB_XREF=gi:8999874 /DB_XREF=est:wd3905..x1 /CLONE_IMAGE:23305533 /UG=Hs.286145 SRB7 (suppressor of RNA polymerase B, yeast) homolog /FL=gb:U6831..1 qb:NM_004264..1
203983_at	gb:NM_005939.1 /DEF=Homo sapiens translin-associated factor X (TSNAX) , mRNA. /FEA=mRNA /GEN=TSNAX /PROD-translin-associated factor X /FL=gb:NM_005939..1
212074_at	Consensus includes qb:BE972774 /FEA=EST /DB_XREF=gi:10586110 /DB_XREF=est:601652004F1 /CLONE_IMAGE:3935281 /UG=Hs.7531 KIAA0810 protein /FL=gb:NM_013229..1 /DEF=Homo sapiens apoptotic protease activating factor (APAF1), transcript variant 1, mRNA. /FEA=mRNA /GEN=APAF1 /PROD-apoptotic protease activating factor isoform a /DB_XREF=gi:7108332 /UG=Hs.77519 apoptotic protease activating factor /FL=gb:AB07813..1 qb:AF134397..1 qb:NM_013229..1
205707_at	gb:NM_014339.1 /DEF=Homo sapiens interleukin 17 receptor (IL17R) , mRNA. /FEA=mRNA /GEN=IL17R /PROD=interleukin 17 receptor /DB_XREF=gi:7657229 /UG=Hs.129751 interleukin 17 receptor /FL=gb:NM_014339..1
218716_x_at	gb:NM_012423.1 /DEF=Homo sapiens CGI-02 protein (CGI-02) , mRNA. /FEA=mRNA /GEN=CGI-02 /PROD=CGI-02 protein /DB_XREF=gi:6912299 /UG=Hs.33979 CGI-02 protein /FL=gb:AF319422..1 qb:AF132937..1 qb:NM_012423..1
217940_s_at	gb:NM_018210.1 /DEF=Homo sapiens hypothetical protein FLJ10769 (FLJ10769) , mRNA. /FEA=mRNA /GEN=FLJ10769 /PROD=hypothetical protein FLJ10769 /DB_XREF=gi:3922653 /UG=Hs.8083 hypothetical protein FLJ10769 /FL=gb:AF151017..1 qb:NM_018210..1
219802_at	gb:NM_024834.1 /DEF=Homo sapiens hypothetical protein FLJ22028 (FLJ22028) , mRNA. /FEA=mRNA /GEN=FLJ22028 /PROD=hypothetical protein FLJ22028 /DB_XREF=gi:13376278 /UG=Hs.192570 hypothetical protein FLJ22028 /FL=gb:NM_024854..1
209259_s_at	gb:AF020043..1 /DEF=Homo sapiens chromosome-associated polypeptide (HCAP) mRNA, complete cds. /FEA=mRNA /GEN=HCAP /PROD=chromosome-associated polypeptide /DB_XREF=gi:3089367 /UG=Hs.241485 chondroitin sulfate proteoglycan 6 (bamacan) /FL=gb:AE020043..1 qb:NM_005445..1 qb:AF067153..1
212037_at	Consensus includes qb:BF508848 /FEA=EST /DB_XREF=gi:11592146 /DB_XREF=est:U1-H-B14-aor-e-06-0-UT.s1 /CLONE_IMAGE:3085907 /UG=Hs.44499 painin, demosome-associated protein
211053_s_at	gb:BC006403..1 /DEF=Homo sapiens NCK adaptor protein 1, clone MSC:12668, mRNA, complete cds. /FEA=mRNA /PROD=NCK adaptor protein 1 /DB_XREF=gi:1.3623576 /FL=gb:BC006403..1
203791_at	gb:NM_005309..2 /DEF=Homo sapiens Dmx-like 1 (DMXL1) , mRNA. /FEA=mRNA /GEN=DMXL1 /PROD=Dmx-like 1 /DB_XREF=gi:9961348 /UG=Hs.181042 Dmx-like 1 /FL=gb:NM_005309..2
203405_at	gb:NM_003720..1 /DEF=Homo sapiens Down syndrome critical region gene 2 (DSCR2) , mRNA. /FEA=mRNA /GEN=DSCR2 /PROD=Down syndrome critical region protein 2 /DB_XREF=gi:1505022 /UG=Hs..5198 Down syndrome critical region gene 2 (DSCR2) , mRNA. /FEA=mRNA /GEN=DSCR2 /PROD=Down syndrome critical subunit 1 /DB_XREF=gi:4505316 /UG=Hs.16513 myosin phosphatase, target subunit 1 /FL=gb:BC03619..1 qb:NM_003720..1
201604_s_at	gb:NM_014153..1 /DEF=Homo sapiens HSPC055 protein (HSPC055) , mRNA. /FEA=mRNA /GEN=HSPC055 /PROD=HSPC055 protein /DB_XREF=gi:7661761 /UG=Hs.1758998 HSPC055 protein /FL=gb:AF161540..1 qb:NM_014153..1
218348_s_at	gb:NM_014071..1 /DEF=Homo sapiens histone deacetylase 7B (HDAC7B-PENDING) , mRNA. /FEA=mRNA /GEN=HDAC7B-PENDING /PROD=histone deacetylase 7B /DB_XREF=gi:1662279 /UG=Hs.116753 histone deacetylase 7B (HDAC7B-PENDING) , mRNA. /FEA=mRNA /GEN=HDAC7B-PENDING /PROD=histone deacetylase 7B
202268_s_at	gb:NM_003905..1 /DEF=Homo sapiens amyloid beta precursor protein-binding protein 1, 59kD (APPBP1) , mRNA. /FEA=mRNA /GEN=APPBP1 PROD=amyloid beta precursor protein-binding protein1 /DB_XREF=gi:4502168 /UG=Hs.61828 amyloid beta precursor protein-binding protein 1,

	59KD / <i>FEA</i> =gb:AL136798.1 <i>gb</i> =BC000480.1 <i>gb</i> =U50939.1 <i>gb</i> =NM_003905.1
202399_s_at	<i>gb</i> :NM_005829.1 / <i>DEF</i> =Homo sapiens adaptor-related protein complex 3, sigma 2 subunit /DB_XREF=gi:5031580 /UG-Hs_154782 adaptor-related protein complex 3, sigma 2 subunit / <i>FEA</i> =mRNA / <i>GEN</i> =AP3S2 / <i>PROD</i> =adaptor-related protein complex 3, sigma 2 subunit / <i>FEI</i> =gb:BC002785.1 <i>gb</i> :NM_005829.1
218515_at	<i>gb</i> :NM_016631.1 / <i>DEF</i> =Homo sapiens hypothetical protein /LOC51395 / <i>FEA</i> =mRNA / <i>GEN</i> =LOC51395 / <i>PROD</i> =hypothetical protein /DB_XREF=gi:17706175 /UG-Hs_26461 hypothetical protein / <i>FEI</i> =gb:AF208862.1 <i>gb</i> :NM_016631.1
209180_at	<i>gb</i> :D49245.1 / <i>DEF</i> =Human geranylgeranyl transferase type II beta-subunit mRNA, complete cds. / <i>FEA</i> =mRNA / <i>PROD</i> =geranylgeranyl transferase type II beta-subunit /DB_XREF=gi:1216503 /UG-Hs_78968 Rab geranylgeranyltransferase, beta subunit / <i>FEI</i> =gb:D49245.1 <i>gb</i> :NM_004582.1
205105_at	<i>gb</i> :NM_002372.1 / <i>DEF</i> =Homo sapiens alpha, class 2A, member 1 (MAN2A1), mRNA. / <i>FEA</i> =mRNA / <i>GEN</i> =MAN2A1 / <i>PROD</i> =mannosidase, alpha, class 2A, member 1 / <i>FEI</i> =gb:U31520.1 <i>gb</i> :NM_002372.1 <i>gb</i> :D63998.1
200666_s_at	<i>gb</i> :NM_006145.1 / <i>DEF</i> =Homo sapiens heat shock 40kD protein 1 (HSPF1), mRNA. / <i>FEA</i> =mRNA / <i>GEN</i> =HSPF1 / <i>PROD</i> =heat shock 40kD protein 1 /DB_XREF=gi:15453689 /UG-Hs_826616 Dnaj (Hsp40) homolog, subfamily B, member 1 / <i>FEI</i> =gb:BC002352.1 <i>gb</i> :NM_006145.1 <i>gb</i> :D49547.1
200972_at	<i>gb</i> :BC000704.1 / <i>DEF</i> =Homo sapiens tetraspan 3, clone MGCG:965, mRNA, complete cds. / <i>FEA</i> =mRNA / <i>PROD</i> =tetraspan 3 / <i>FEI</i> =gb:BC000704.1 <i>gb</i> :BC004280.1 <i>gb</i> :AF054840.1 <i>gb</i> :NM_005724.1 <i>gb</i> :AEI33423.1
218352_at	<i>gb</i> :NM_018191.1 / <i>DEF</i> =Homo sapiens hypothetical protein FLJ0716 (FLJ10116), mRNA. / <i>FEA</i> =mRNA / <i>GEN</i> =FLJ10716 / <i>PROD</i> =hypothetical protein FLJ0716 /DB_XREF=gi:8922616 /UG-Hs_100090 tetraspan 3 / <i>FEI</i> =gb:BC000704.1 <i>gb</i> :BC004280.1 <i>gb</i> :AF054840.1 <i>gb</i> :NM_005724.1 <i>gb</i> :AEI33423.1
217728_at	<i>gb</i> :NM_014624.2 / <i>DEF</i> =Homo sapiens S100 calcium-binding protein A6 (calcycillin) (S100A6), mRNA. / <i>FEA</i> =mRNA / <i>GEN</i> =S100A6 / <i>PROD</i> =S100 calcium-binding protein A6 / <i>FEI</i> =gb:BC004280.1 <i>gb</i> :AF054840.1 <i>gb</i> :NM_014624.2
211971_s_at	Consensus includes <i>gb</i> :AI653608 / <i>FEI</i> =EST /DB_XREF=gi:41737587 / <i>DB</i> _XREF=est:zz1a06.x1 / <i>CLONE</i> =IMAGE:2289202 /UG-Hs_182490 leucine-rich protein mRNA
212500_at	Consensus includes <i>gb</i> :AI049319.1 / <i>DEF</i> =Homo sapiens S100 calcium-binding protein A6 (calcycillin) (S100A6), mRNA. / <i>FEA</i> =mRNA / <i>GEN</i> =FLJ22329 (FLJ10716) / <i>PROD</i> =hypothetical protein / <i>FEI</i> =gb:BC004280.1 <i>gb</i> :AF054840.1 <i>gb</i> :NM_014624.2
218473_s_at	<i>gb</i> :NM_024656.1 / <i>DEF</i> =Homo sapiens hypothetical protein FLJ22329 (FLJ22329) / <i>FEI</i> =gb:NM_024656.1
203580_s_at	<i>gb</i> :NM_003983.1 / <i>DEF</i> =Homo sapiens solute carrier family 7 (cationic amino acid transporter, Y+ system), member 6 (SLC7A6), mRNA. / <i>FEI</i> =mRNA / <i>GEN</i> =SLC7A6 / <i>PROD</i> =signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 / <i>FEA</i> =mRNA / <i>GEN</i> =SLC7A6 / <i>PROD</i> =signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 / <i>FEI</i> =gb:NM_003983.1
200900_s_at	Carrier family 7 (cationic amino acid transporter, Y+ system), member 6 / <i>FEI</i> =gb:D8442.1 <i>gb</i> :NM_003983.1
221652_s_at	Consensus includes <i>gb</i> :AI583537 / <i>FEI</i> =EST /DB_XREF=gi:45469434 / <i>DB</i> _XREF=est:ts12d03.x1 / <i>CLONE</i> =IMAGE:2228357 /UG-Hs_75709 mannose-6'-phosphate receptor (cation dependent) / <i>FEI</i> =gb:NM_002355.2 <i>gb</i> :M16985.1
EL110637	<i>gb</i> :AF274950.1 / <i>DEF</i> =Homo sapiens PNAS-25 mRNA, complete cds. / <i>FEA</i> =mRNA / <i>PROD</i> =PNAS-25 / <i>DB</i> _XREF=gi:12751064 /UG-Hs_22595 hypothetical protein
217750_s_at	<i>gb</i> :NM_023079.1 / <i>DEF</i> =Homo sapiens hypothetical protein FLJ13855 (FLJ13855), mRNA. / <i>FEA</i> =mRNA / <i>GEN</i> =FLJ13855 / <i>PROD</i> =hypothetical protein FLJ13855 / <i>FEI</i> =gb:NM_023079.1
203544_s_at	Consensus includes <i>gb</i> :AV615149.1 /UG-Hs_168232 hypothetical protein FLJ13855 / <i>FEI</i> =gb:NM_023079.1 / <i>DB</i> _XREF=est:AV615179 / <i>CLONE</i> =GKRAE05 / <i>UG</i> =beta precursor / <i>PROD</i> =signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 / <i>FEA</i> =mRNA / <i>GEN</i> =STAM / <i>GEN</i> =003473.1 / <i>PROD</i> =signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 / <i>FEI</i> =gb:AF017782.1 <i>gb</i> :NM_003473.1
221580_s_at	<i>gb</i> :BC001972.1 / <i>DEF</i> =Homo sapiens Clone MGCG:15306, mRNA, complete cds. / <i>FEA</i> =mRNA / <i>PROD</i> =Unknown (protein for MGCG:5306) / <i>DB</i> _XREF=gi:12805036 / <i>FEI</i> =gb:NM_301132 hypothetical protein MGCG:306 / <i>FEI</i> =gb:BC001972.1
202629_at	Consensus includes <i>gb</i> :AV615157.9 / <i>FEI</i> =EST /DB_XREF=gi:10283342 / <i>DB</i> _XREF=est:AV615179 / <i>CLONE</i> =GKRAE05 / <i>UG</i> =beta precursor protein (cytoplasmic tail)-binding protein 2 / <i>FEI</i> =gb:AF017782.1 <i>gb</i> :NM_006380.1
205763_s_at	<i>gb</i> :NM_006173.2 / <i>DEF</i> =Homo sapiens DEADH (Asp-Glu-Ala-AspHs) box polypeptide 18 (Myo-regulated) (DDX18), mRNA. / <i>FEA</i> =mRNA / <i>GEN</i> =DDX18 / <i>PROD</i> =DEADH (Asp-Glu-Ala-AspHs) box polypeptide 18 / <i>DB</i> _XREF=gi:111131299 / <i>DB</i> _XREF=est:7q93e05.x1 / <i>CLONE</i> =IMAGE:3704936 / <i>UG</i> =Asp-Glu-Ala-AspHs box polypeptide 18 (Myo-regulated) / <i>FEI</i> =gb:NM_006173.2
212337_at	Consensus includes <i>gb</i> :AI687738 / <i>FEI</i> =EST /DB_XREF=est:tp93908.x1 / <i>CLONE</i> =IMAGE:2206910 / <i>UG</i> =Hs_699 peptidyld-prolyl isomerase B (cyclophilin B)
212244_at	Consensus includes <i>gb</i> :AI050091.1 / <i>DEF</i> =Homo sapiens mRNA; cDNA DKTP586F1918 (from clone DKTP586F1918); partial cds. / <i>FEA</i> =mRNA / <i>GEN</i> =DKTP586F1918 / <i>PROD</i> =hypothetical protein / <i>FEI</i> =gb:488411.1 / <i>FEA</i> =mRNA / <i>GEN</i> =DKTP586F1918 protein
222011_s_at	Consensus includes <i>gb</i> :BF224073 / <i>FEI</i> =EST /DB_XREF=gi:111131299 / <i>DB</i> _XREF=est:7q93e05.x1 / <i>CLONE</i> =IMAGE:3704936 / <i>UG</i> =Hs_278544 acetyl-Coenzyme A acetyltransferase 2 (acetobutyryl Coenzyme A thioesterase)
204725_s_at	<i>gb</i> :NM_006153.1 / <i>DEF</i> =Homo sapiens NCK adaptor protein 1 (NCK1), mRNA. / <i>FEA</i> =mRNA / <i>GEN</i> =NCK1 / <i>PROD</i> =NCK adaptor protein 1 / <i>DB</i> _XREF=gi:1:5453753 / <i>UG</i> =Hs_54589 NCK adaptor protein 1 / <i>FEI</i> =gb:NM_006153.1

208860_s_at	gb:U09820.1 /DEF=Human helicase II (RAD54L) mRNA, complete cds. /FEA=mRNA /GEN=RAD54L /PROD=helicase II /DB_XREF=gi:606832 /UG=Hs.96264 alpha thalassemial retardation X-linked (RAD54 (S. cerevisiae) homolog) /FI=gb:U09820.1 qb:NM_000489.1 qb:NM_000489.1
203224_at	Consensus includes gb:SF340123 /FEA=EST /DB_XREF=gi:11286595 /DB_CLONE=IMAGE:602037283F1 /CLONE=
in FLJ11149 /FI=gb:NM_018339.1	/DB_XREF=est:602037283F1 /CLONE=IMAGE:4185212 /UG=Hs.37558 hypothetical protein
gb:I40326_1 /DEF=Homo sapiens Hepatitis B virus X-associated protein 1 mRNA, complete cds. /FEA=mRNA /PROD=X-associated protein 1	/DB_XREF=gi:6953361 /
208619_at	Ug=Ts.108327 damage-specific DNA binding protein 1 (127kD) /FI=gb:U18299.1 qb:U32986.1 qb:NM_001923.2 qb:140326.1
208765_s_at	Consensus includes gb:NM_005826.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein R (hnRNP _R) mRNA. /FEA=mRNA /GEN=hnRNP _R /PROD=heterogeneous nuclear ribonucleoprotein R /DB_XREF=gi:5031754 /UG=Hs.15265 heterogeneous nuclear ribonucleoprotein R
220832_at	/FI=gb:BC001449.1 qb:AF000364.1 qb:NM_005826.1
gb:NM_016610.1 /DEF=Homo sapiens toll-like receptor 8 (LOC51311), mRNA. /FEA=mRNA /GEN=LOC51311 /PROD=Toll-like receptor 8	/DB_XREF=gi:7706147 /
208398_s_at	Ug=Ts.272410 Toll-like receptor 8 /FI=gb:AF246971.1 qb:NM_016610.1 qb:AF245703.1
gb:NM_004865.1 /DEF=Homo sapiens TBP-like 1 (TBPL1), mRNA. /FEA=mRNA /GEN=TBPL1 /PROD=TBP-like 1 /DB_XREF=gi:4759233 /UG=Hs.13993 TBP-like 1 /FI=gb:AF130312.1 qb:NM_004865.1	
205077_s_at	gb:NM_002613.1 /DEF=Homo sapiens phosphatidylinositol glycan, class F (PIGF), mRNA. /FEA=mRNA /GEN=PIGF /PROD=phosphatidylinositol glycan, class F /DB_XREF=gi:14505796 /UG=Hs.166382 phosphatidylinositol glycan, class F /FI=gb:DI3435.1 qb:NM_002643.1
210616_s_at	gb:AB020712.1 /DEF=Homo sapiens mRNA for KIAA0905 protein, complete cds. /FEA=mRNA /GEN=KIAA0905 /PROD=KIAA0905 protein /DB_XREF=gi:4240298 /UG=Hs.10266 yeast Sec31P homolog /FI=gb:AB020712.1
211761_s_at	gb:BC005975.1 /DEF=Homo sapiens calcyclin binding protein, clone MGC:14660, mRNA, complete cds. /FEA=mRNA /PROD=calcyclin binding protein /DB_XREF=gi:13543650 /FI=gb:BC005975.1
213164_at	Consensus includes gb:AI867198 /FEA=EST /DB_XREF=gi:5540214 /DB_XREF=est:wa01c11.x1 /CLONE=IMAGE:2296820 /UG=Hs.324787 solute carrier family 5 (inositol transporters), member 3 /FI=gb:NM_005933.1
219940_s_at	gb:NM_018386.1 /DEF=Homo sapiens hypothetical protein FLJ11305 (FLJ11305), mRNA. /FEA=mRNA /GEN=FLJ11305 /PROD=hypothetical protein FLJ11305 /DB_XREF=gi:5922386 /UG=Hs.7049 hypothetical protein FLJ11305 /FI=gb:NM_018386.1
203800_s_at	Consensus includes gb:BG254653 /FEA=EST /DB_XREF=gi:1276469 /DB_XREF=est:602368321F1 /CLONE=IMAGE:4476773 /UG=Hs.247324 hypothetical protein LOC63931 /FI=gb:NM_022100.1
213026_at	Consensus includes gb:BE965998 /FEA=EST /DB_XREF=gi:11770950 /DB_XREF=gi:11770950 /DB_XREF=est:601659892R1 /CLONE=IMAGE:3905710 /UG=Hs.264482 Apo12 (autophagy 12, S. cerevisiae)-like
215165_x_at	Consensus includes gb:AL080099.1 /DEF=Homo sapiens mRNA; cDNA DKZP56AG1272 (from clone DKZP56AG1272); partial cds. /FEA=mRNA /GEN=CTNN1 /PROD=catenin, delta 1 (CTNN1), mRNA. /FEA=mRNA /GEN=CTNN1 /PROD=catenin, delta 1 /FI=gb:NM_001331.1
202864_s_at	gb:NM_003113.1 /DEF=Homo sapiens nuclear antigen Sp100 (SP100), mRNA. /FEA=mRNA /GEN=SP100 /PROD=nuclear antigen Sp100 /DB_XREF=gi:4507164 /UG=Hs.77617 nuclear antigen Sp100 /FI=gb:M60618.1 qb:NM_003113.1
208407_s_at	gb:NM_001331.1 /DEF=Homo sapiens catenin (cadherin-associated protein), delta 1 (CTNN1), mRNA. /FEA=mRNA /GEN=CTNN1 /PROD=catenin, delta 1 (CTNN1), mRNA. /FEA=mRNA /GEN=FVT1 /PROD=follicular lymphoma transferase and orotidine-5'-decarboxylase
202419_at	variant translocation 1 /DB_XREF=gi:503816 /UG=Is.74050 follicular lymphoma variant translocation 1 (FVT1), mRNA. /FEA=mRNA /GEN=FVT1 /PROD=follicular lymphoma variant translocation 1 /FI=gb:NM_002035.1
201833_at	gb:NM_001527.1 /DEF=Homo sapiens histone deacetylase 2 (HDAC2), mRNA. /FEA=mRNA /GEN=HDAC2 /PROD=histone deacetylase 2 /DB_XREF=gi:4557640 /UG=Hs.3332 histone deacetylase 2 /FI=gb:U31814.1 qb:NM_001527.1
217879_at	Consensus includes gb:AI566824 /FEA=EST /DB_XREF=gi:12919571 /DB_XREF=est:AU566824 /CLONE=C50DF025IN03 (3 prime) /UG=Hs.177405 cell division cycle 27 /FI=gb:NM_001256.1

Tabelle 5: Gene aus Clusteranalyse 5

Affymetrix-Beschreibung der Sequenz in der Genebank Datenbank interne Bezeichnung	
201466_s_at	gb:NM_002228.2 /DEF=Homo sapiens v-jun avian sarcoma virus 17 oncogene homolog (JUN), mRNA. /FEA=mRNA /GEN=JUN /PROD=v-jun avian sarcoma virus 17 oncogene homolog /BL=gb:BC002616.1 gb:NM_002228.2
202425_x_at	gb:NM_000944.1 /DEF=Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PP3CA), mRNA. /FEA=mRNA /GEN=PPP3CA /PROD=protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) /DB_XREF=gi:6715567 /DC=Hs-272458 protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) /EL=gb:J05480.1 gb:J1478.1
218566_s_at	gb:NM_000944.1 gb:AL553950.1
	gb:NM_012124.1 /DEF=Homo sapiens chord domain-containing protein 1 (CHPL), mRNA. /FEA=mRNA /GEN=CHPL /PROD=chord domain-containing protein 1 /DB_XREF=gi:5912303 /UG=Hs-22857 cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1 /EL=gb:AF192466.1
214349_at	gb:NM_012124.1
	Consensus includes gb:AV764378 /FEA=EST /DB_XREF=est:10922226 /DB_XREF=est:AV764378 /CLONE=MDSAGE03 /UG=Hs_163863 ESTs. Moderately similar to
204314_s_at	POU2_HUMAN RETROVIRUS-RELATED POU POLYPROTEIN H_sapiens binding /DB_XREF=gi:158053 /UG=Hs_7919 GMP responsive element binding protein 1 (CREB1), mRNA. /FEA=mRNA /GEN=CREB1 /PROD=GMP responsive element binding protein 1 /EL=gb:M27691.1 gb:NM_004379.1
208753_s_at	gb:BC002387.1 /DEF=Homo sapiens nucleosome assembly protein 1-like 1, clone MGC:8688, mRNA, complete cds. /FEA=mRNA /PROD=nucleosome assembly protein 1-like 1 /DB_XREF=gi:12803166 /UG=Hs-170662 nucleosome assembly protein 1-like 1 /EL=gb:BC002387.1 gb:ALL62068.1
215452_x_at	Consensus includes gb:AL031133 /DEF=Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs. S
204119_s_at	gb:US0339.1 /DEF=Human adenosine kinase short form mRNA, complete cds. /FEA=mRNA /PROD=adenosine kinase short form /DB_XREF=gi:11906010 /DC=Hs_94382 adenosine kinase /EL=gb:U50196.1 gb:090339.1 gb:NM_001123.1
201304_at	gb:NM_005000.2 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (NDUEA5), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=NDUEA5 /PROD=NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (NDUEA5) /DB_XREF=gi:1369821 /DC=Hs_83916 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (NDUEA5) /EL=gb:U53468.1 gb:U64028.1
218131_s_at	gb:NM_017660.1 /DEF=Homo sapiens hypothetical protein FLJ20085 (FLJ20085), mRNA. /FEA=mRNA /GEN=FLJ20085 /PROD=hypothetical protein FLJ20085 /DB_XREF=gi:8923093 /UG=Hs_118964 hypothetical protein FLJ20085 /EL=gb:NM_017660.1
201788_at	gb:NM_007372.1 /DEF=Homo sapiens RNA helicase-related protein (RNAPII), mRNA. /FEA=mRNA /GEN=RNAPII /PROD=RNA helicase-related protein /DB_XREF=gi:11321631 /UG=Hs_8765 RNA helicase-related protein /EL=gb:NM_007372.1 gb:AF083255.1
209780_at	gb:AL136883.1 /DEF=Homo sapiens mRNA; cDNA DKFp43AD166 (from clone DKFp43AD166); complete cds. /FEA=mRNA /GEN=DKFp43AD166 /PROD=hypothetical protein DKFp56AE013 /EL=gb:ALL36883.1
219375_at	gb:NM_006090.1 /DEF=Homo sapiens cholineethanolaminephosphotransferase (CEET1), mRNA. /FEA=mRNA /GEN=CEET1 /PROD=cholineethanolaminephosphotransferase /EL=gb:NM_006090.1
209187_at	Consensus includes gb:AW516932 /FEA=EST /DB_XREF=gi:7154941 /DB_XREF=est:109405.x1 /CLONE-IMAGE:2748848 /UG=Hs_16669 down-regulator of transcription 1, TBP-binding (negative cofactor 2) /EL=gb:IC002809.1
219279_at	gb:NM_017716.1 /DEF=Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA. /FEA=mRNA /GEN=FLJ20220 /PROD=hypothetical protein FLJ20220 /DB_XREF=gi:8923209 /UG=Hs_21126 hypothetical protein FLJ20220 /EL=gb:NM_017716.1
206976_s_at	gb:NM_006644.1 /DEF=Homo sapiens heat shock 105kd (HSP105B), mRNA. /FEA=mRNA /GEN=HSP105B /PROD=heat shock 105kd /DB_XREF=gi:5729878 /DC=Hs-36927 heat shock 105kd /EL=gb:AB003333.1 gb:NM_006644.1
215596_s_at	Consensus includes gb:AL163248 /DEF=Homo sapiens chromosome 21 segment HS21C048 /FEA=mRNA_2 /DB_XREF=gi:7717304 /UG=Hs_288773 zinc finger protein 294
	Consensus includes gb:AU270770 /DEF=Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exon 1 and joined CDS features /FEA=mRNA_1 /DB_XREF=gi:9189625 /UG=Hs_283857 Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exon 1 and joined CDS fea-
216511_s_at	

turus				
201889_at	gb NM_014888.1 /DEF=Homo sapiens predicted osteoblast protein (GS3786), mRNA. /FEA=mRNA /GEN=GS3786 /PROD=predicted osteoblast protein /DB_XREF=gi:7661713 /UG-Hs.29882 predicted osteoblast protein /EL=gb:DB120.1 /gb:NM_014888.1			
201435_s_at	Consensus includes gb:AW266640 /FEA=EST /DB_XREF=gi:6655670 /DB_XREF=est:xv52a03.x1 /CLONE=IMAGE:2816716 /UG-Hs.79306 eukaryotic translation initiation factor 4E /FE=gb:ML353.1 /gb:NW_001968.1			
212232_at	Consensus includes gb:AB02231.1 /DEF=Homo sapiens mRNA for KIAA1014 protein, partial cds. /FEA=mRNA /GEN=KIAA1014 /PROD=KIAA1014 protein /DB_XREF=gi:4589677 /UG-Hs.6834 KIAA1014 protein			
214329_x_at	Consensus includes gb:AW474434 /FEA=EST /DB_XREF=gi:7044540 /DB_XREF=est:xs95f07.x1 /CLONE=IMAGE:2777437 /UG-Hs.301527 ESTs, moderately similar to unknown H.sapiens			
212099_at	Consensus includes gb:AL263909 /FEA=EST /DB_XREF=gi:3872112 /DB_XREF=est:q108f09.x1 /CLONE=IMAGE:1855913 /UG-Hs.204354 ras homolog gene family member B /FE=gb:NM_004040.1			
213618_at	Consensus includes gb:AB011152.1 /DEF=Homo sapiens mRNA for KIAA0580 protein, partial cds. /FEA=mRNA /GEN=KIAA0580 /PROD=KIAA0580 protein /DB_XREF=gi:13041683 /UG-Hs.22572 KIAA0580 protein			
216899_s_at	Consensus includes gb:AC003999 /DEF=Human PAC clone RP5-1139P1 from 7p15-p21 /FEA=CDs /DB_XREF=q1:12772566 /UG-Hs.52644 SKAP55 homologue			
201437_s_at	gb NM_001968.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4E (EIF4E), mRNA. /FEA=mRNA /GEN=EIF4E /PROD=eukaryotic translation initiation factor 4E /DB_XREF=gi:4503534 /UG-Hs.79306 eukaryotic translation initiation factor 4E /EL=gb:NM_001968.1			
212122_at	Consensus includes gb:AW7711590 /FEA=EST /DB_XREF=gi:7703617 /DB_XREF=est:in589308.x1 /CLONE=IMAGE:3032126 /UG-Hs.166982 phosphatidylinositol glycan, class F			
208666_s_at	Consensus includes gb:BE86412 /FEA=EST /DB_XREF=gi:103165097 /DB_XREF=est:601678667f1 /CLONE=IMAGE:3961522 /UG-Hs.119222 suppression of tumorigenicity 13 (colon carcinoma) (Hsp70-Interacting protein) /EL=gb:AF116650.1			
2118252_at	gb NM_018204.1 /DEF=Homo sapiens cytoskeleton associated protein 2 (CKAP2), mRNA. /FEA=mRNA /GEN=CKAP2 /PROD=cytoskeleton associated protein 2 /DB_XREF=gi:8922641 /UG-Hs.24641 cytoskeleton associated protein 2 /EL=gb:AL136849.1 /gb:NM_018204.1			
2116384_x_at	Consensus includes gb:AF257099 /DEF=Homo sapiens prothymosin alpha (PTMA) gene, complete cds /FEA=mRNA /GEN=PTMA			
217100_s_at	Consensus includes gb:AK026451.1 /DEF=Homo sapiens cDNA: FLJ22798 fis, Clone KIAA2617. /FEA=mRNA /DB_XREF=gi:10439320 /UG-Hs.127287 KIAA0794 protein			
204313_s_at	Consensus includes gb:AA1614846 /FEA=EST /DB_XREF=gi:1735796 /DB_XREF=est:2q4209.s1 /CLONE=IMAGE:632359 /UG-Hs.79194 cAMP responsive element binding protein 1 /EL=gb:NM_27691.1 /gb:NM_004379.1			
2114257_s_at	Consensus includes gb:AB890010 /FEA=EST /DB_XREF=gi:3016889 /DB_XREF=est:aj89t08.s1 /CLONE=IMAGE:1403679 /UG-Hs.50785 SEC22, vesicle trafficking protein (S. cerevisiae)-like 1			
218595_s_at	gb NM_018072.1 /DEF=Homo sapiens hypothetical protein FLJ10359 (FLJ10359), mRNA. /FEA=mRNA /GEN=FLJ10359 /PROD=hypothetical protein FLJ10359 /DB_XREF=gi:8922377 /UG-Hs.285861 hypothetical protein FLJ10359 /EL=gb:NM_018072.1			
213128_s_at	Consensus includes gb:AB527499 /FEA=EST /DB_XREF=gi:2269568 /DB_XREF=est:ng4f07.s1 /CLONE=IMAGE:937381 /UG-Hs.301667 Homo sapiens mRNA; CDN DKTP566103 (from clone DKF25566104)			
207719_x_at	gb NM_014812.1 /DEF=Homo sapiens KIAA0470 gene product (KIAA0470), mRNA. /FEA=mRNA /GEN=KIAA0470 /PROD=KIAA0470 /DB_XREF=gi:766141 /gb:NM_25132 KIAA0470 gene product /EL=gb:AB022657.1 /gb:NM_014812.1			
200060_s_at	gb BC001639.1 /DEF=Homo sapiens, RNA-binding protein S1, serine-rich domain, clone NCG:1125, mRNA, complete cds. /FEA=mRNA /PROD=RNA-binding protein S1, serine-rich domain /DB_XREF=gi:12804496 /UG-Hs.75104 RNA-binding protein S1, serine-rich domain /EL=gb:BC001659.1 /gb:BC001838.1			
200634_at	gb NM_005022.1 /DEF=Homo sapiens profilin 1 (FEN1), mRNA. /FEA=mRNA /GEN=PFN1 /PROD=profilin 1 /DB_XREF=gi:4826897 /UG-Hs.75721 profilin 1 /EL=gb:BC002475.1 /gb:NM_005022.1			
2020770_s_at	gb NM_004354.1 /DEF=Homo sapiens cyclin G2 (CCNG2), mRNA. /FEA=mRNA /GEN=CCNG2 /PROD=cyclin G2 /DB_XREF=gi:1757935 /UG-Hs.79069 cyclin G2 /EL=gb:U74714.1 /gb:NM_004354.1			
20201008_s_at	Consensus includes gb:AA162232 /FEA=EST /DB_XREF=gi:2881843 /DB_XREF=est:ob84h09.s1 /CLONE=IMAGE:1338113 /UG-Hs.179526 upregulated by 1,25-dihydroxyvitamin D-3 /EL=gb:NM_006412.1 /gb:SL73591.1			
21218534_s_at	gb NM_018046.1 /DEF=Homo sapiens hypothetical protein FLJ10263 (FLJ10263), mRNA. /FEA=mRNA /GEN=FLJ10263 /PROD=hypothetical protein FLJ10263			

200933_at	Consensus includes gb:BA939270 / FER=EST / DB_XREF=gi:3099183 / DB_XREF=est:0031b02.s1 / CLONE=IMAGE:1587915 / UG=Hs_5151 RAN binding protein 7 / EL=gb:ATU98199.1 qb:NM_006391.1
214202_at	Consensus includes gb:AK023737.1 / DEF=Homo sapiens cDNA FLJ13675 fls, clone PLACE1011875, highly similar to Homo sapiens mRNA for KIAA0580 protein. / FEA=mRNA / DB_XREF=gi:10435758 / UG=Hs_287588 Homo sapiens cDNA FLJ13675 fls, clone PLACE1011875, highly similar to Homo sapiens mRNA for KIAA0580 protein.
213704_at	Consensus includes gb:AA129753 / FER=EST / DB_XREF=gi:11690163 / DB_XREF=est:z116a12.s1 / CLONE=IMAGE:502078 / UG=Hs_78948 Rab geranylgeranyltransf erase, beta subunit
212357_at	Consensus includes gb:AL799061 / FER=EST / DB_XREF=gi:53364533 / DB_XREF=est:we98a10.x1 / CLONE=IMAGE:2349114 / UG=Hs_6048 FEM-1 (C.elegans) homolog b / EL=gb:AC178632.1 qb:NM_015322.1
201873_s_at	gb:NM_002940.1 / DEF=Homo sapiens ATP-binding cassette, sub-family E (ORBP), member 1 (ABCE1), mRNA, / FEAT=mRNA / GEN=ABCE1 / PROD=ATP-binding cassette, sub-family E, member 1. / DB_XREF=gi:4506558 / UG=Hs_12013 ATP-binding cassette, sub-family E (ORBP), member 1 / EL=gb:NM_002940.1
218618_s_at	gb:NM_022763.1 / DEF=Homo sapiens hypothetical protein FLJ23399 (FLJ23399), mRNA, / FEAT=mRNA / GEN=FLJ23399 / PROD=hypothetical protein FLJ23399 / DB_XREF=gi:12222434, / UG=Hs_299883 hypothetical protein FLJ23399 / EL=gb:NM_022763.1
203689_s_at	Consensus includes gb:AT743037 / FER=EST / DB_XREF=gi:5111325 / DB_XREF=est:98505.x1 / CLONE=IMAGE:23711881 / UG=Hs_89764 fragile X mental retardation 1 / EL=gb:NM_002024.1
201074_at	Consensus includes gb:DA593083 / FER=EST / DB_XREF=gi:2109333 / DB_XREF=est:un16d01.s1 / CLONE=IMAGE:1084033 / UG=Hs_172280 SMN1 related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 / EL=gb:NM_066651.5 qb:NM_003074.1
200778_s_at	Consensus includes gb:AA119427 / FER=EST / DB_XREF=gi:3142636 / DB_XREF=est:4e4803.x1 / CLONE=IMAGE:1742260 / UG=Hs_155595 neural precursor cell expressed, developmentally down-regulated 5 / EL=gb:D25401.1 qb:NM_004410.1 qb:D63978.1
202307_s_at	gb:NM_000593.2 / DEF=Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 2 (ABC2B1), mRNA, / FEAT=mRNA / GEN=ABC2B2 / PROD=ATP-binding cassette, sub-family B (MDR/TAP), member 2 / EL=gb:NM_021204.1
213145_at	Consensus includes gb:BF001666 / FER=EST / DB_XREF=gi:10701941 / DB_XREF=est:7991d12.x1 / CLONE=IMAGE:3313847 / UG=Hs_12460 Homo sapiens clone 23810 tRNA sequence
216588_s_at	gb:NM_018691.1 / DEF=Homo sapiens chromosome 5 open reading frame 3 (CSORE3), mRNA, / FEAT=mRNA / GEN=C50RF3 / PROD=hypothetical protein / DB_XREF=gi:8922068 / UG=Hs_166551 chromosome 5 open reading frame 3 / EL=gb:NM_018691.1
217834_s_at	gb:NM_006312.1 / DEF=Homo sapiens NS1-associated protein 1 (NS1AP1), mRNA, / FEAT=mRNA / GEN=NS1AP1 / PROD=NS1-associated protein 1 / DB_XREF=gi:15453805 / UG=Hs_155649 NS1-associated protein 1 / EL=gb:AF1155568.1 qb:NM_005372.1
205038_at	Consensus includes gb:BG5540504 / FER=EST / DB_XREF=gi:115323737 / DB_XREF=est:602569230F1 / CLONE=IMAGE:4693783 / UG=Hs_54452 zinc finger protein subfamily 1A, 1 (Ikaros) / EL=gb:U0462.1 qb:NM_0006060.1
203132_at	gb:NM_000322.1 / DEF=Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1), mRNA, / FEAT=mRNA / GEN=RB1 / PROD=retinoblastoma 1 (including osteosarcoma) / DB_XREF=gi:4506434 / UG=Hs_75770 retinoblastoma 1 (including osteosarcoma) / EL=gb:M33647.1 qb:M28419.1
211297_s_at	gb:NM_000321.1 / DEF=Human protein serine/threonine kinase stk1 mRNA, complete cds, / FEAT=mRNA / PROD=protein serine/threonine kinase / DB_XREF=gi:13484242 / UG=Hs_184236 cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase) / EL=gb:L20320.1
2123375_at	Consensus includes gb:AL5563727 / FER=EST / DB_XREF=est:AL563727 / CLONE=CSDD007YL16 (3 prime) / UG=Hs_306094 trinucleotide repeat containing 12
208986_at	Consensus includes gb:AL559478 / FER=EST / DB_XREF=est:AL559478 / CLONE=CSDD013YM17 (5 prime) / UG=Hs_21704 transcription factor 12 (TIE1, helix-loop-helix transcription factors 4) / EL=gb:M80627.1 qb:MB32233.1 qb:NM_003205.2
211956_s_at	gb:NM_021204.1 / DEF=Homo sapiens E-1 enzyme (MASA), mRNA, / FEAT=mRNA / GEN=MASA / PROD=E-1 enzyme / DB_XREF=gi:10864016 / UG=Hs_18442 E-1 enzyme
214870_x_at	Consensus includes gb:AC002045 / DEF=Human Chromosome 16 BAC clone C19B7SK-A-589H1 / FER=mRNA_2 / DB_XREF=gi:2951945 / UG=Hs_251928 nuclear pore complex interacting protein
209852_x_at	gb:BC001423.1 / DEF=Homo sapiens, Similar to proteaseome (prosome, macropain) 28 subunit 3, clone NCC:1394, mRNA, complete cds, / FEA=mRNA / PROD=similar to proteaseome (prosome, macropain) 28subunit, 3 / DB_XREF=gi:12655138 / UG=Hs_152978 proteasome (prosome, macropain) activator subunit 3 (P28 gamma; K1) / EL=gb:BC001423.1 qb:BC002684.1
209063_x_at	Consensus includes gb:BF248165 / FER=EST / DB_XREF=est:601859364F1 / CLONE=IMAGE:4069886 / UG=Hs_109643 polyadenylate binding protein-interacting protein 1 / EL=gb:AL136920.1
201177_s_at	gb:NM_005199.1 / DEF=Homo sapiens SUMO-1 activating enzyme subunit 2 (UB22), mRNA, / FEAT=mRNA / GEN=UB22 / PROD=SUMO-1 activating enzyme subunit 2 / DB_XREF=gi:4886648 / UG=Hs_4311 SUMO-1 activating enzyme subunit 2 / EL=gb:BC003153.1 qb:U35832.1 qb:AE090384.1 qb:AF079566.1
212264_s_at	gb:AE110957.1 qb:NM_005493.1 qb:NM_005495.1 qb:NM_005495.1 qb:NM_005495.1 / FER=EST / DB_XREF=est:9970161 / DB_XREF=gi:3286484 / UG=Hs_154978 KIAA0261 protein

218878_s_at	gb:NM_012238.3 /DEF=Homo sapiens sirtuin [silent mating type information regulation 2, <i>S. cerevisiae</i> , homolog] 1 /DB_XREF=gi:13775598 /UG=Hs.31176 sirtuin (silent mating type information regulation 2, <i>S. cerevisiae</i> , homolog) 1 /
202163_s_at	gb:NN_004779.1 /DEF=Homo sapiens CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA. /FEA=mRNA /GEN=CNOT8 /PROD=CCNA-NOT transcription complex, subunit 8 /DB_XREF=gi:4758945 /UG=Hs.26703 CCR4-NOT transcription complex, subunit 8 /
203584_at	gb:NM_014673.1 /DEF=Homo sapiens KIAA0103 gene product (KIAA0103), mRNA. /FEA=mRNA /GEN=KIAA0103 /PROD=KIAA0103 gene product /DB_XREF=gi:1661909 /UG=Hs.154387 KIAA0103 gene product /FI=gb:D14659.1_gb:NM_014673.1
201901_s_at	Consensus includes gb:Z14077.1 /DEF=H. sapiens mRNA for YY1NE-EL protein. /FEA=mRNA /PROD=YY1_NE-EL /
213743_at	transcription factor /FI=gb:MT7698.1_gb:M76541.1_gb:NM_003403.2 /DB_XREF=gi:10034660 /DB_XREF=est:7d75b03_x1 /CLONE=IMAGE:13278765 /UG=Hs.155478 cyclin T2
202883_s_at	Consensus includes gb:T79584 /FEA=EST /DB_XREF=gi:698093 /DB_XREF=est:yd71a11_sl /CLONE=IMAGE:113660 /UG=Hs.108705 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform /FEA=mRNA /PROD=PR65 /
202069_s_at	Consensus includes gb:AI826060 /FEA=EST /DB_XREF=gi:5446731 /DB_XREF=est:wk28a12_x1 /CLONE=IMAGE:2413630 /UG=Hs.250616 isocitrate dehydrogenase 3 (NAD+), alpha /FI=gb:NM_00530.1_gb:U0681.1 /DB_XREF=est:ts77a09_x1 /CLONE=GCKEQD03 /UG=Hs.292477 ESTs
222303_at	Consensus includes gb:AV700891 /FEA=EST /DB_XREF=gi:10302862 /DB_XREF=est:AV700891 /CLONE=GCKEQD03 /UG=Hs.292477 ESTs
203102_s_at	gb:NM_002408.2 /DEF=Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT2), mRNA. /FEA=mRNA /GEN=MGAT2 /PROD=paloha-1,6-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase /FI=gb:NM_002408.2
212982_at	Consensus includes gb:AI621223 /FEA=EST /DB_XREF=gi:4630349 /DB_XREF=est:ts77a09_x1 /CLONE=IMAGE:2237272 /UG=Hs.4014 KIAA0946 protein; Huntingtin interacting Protein H
200050_at	gb:NM_007145.1 /DEF=Homo sapiens zinc finger protein 146 (ZNF146), mRNA. /FEA=mRNA /GEN=ZNF146 /PROD=zinc finger protein 146 /DB_XREF=gi:6005965 /UG=Hs.20189 zinc finger protein 146 /FI=gb:BC005154.1_gb:NM_007145.1
202430_s_at	gb:NM_021105.1 /DEF=Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA. /FEA=mRNA /GEN=PLSCR1 /PROD=phospholipid scramblase 1 /DB_XREF=gi:1110863876 /UG=Hs.198282 phospholipid scramblase 1 /FI=gb:NM_021105.1_gb:AB006746.1_gb:AF098642.1
218757_s_at	gb:NM_023010.1 /DEF=Homo sapiens similar to yeast Upf3, variant B (UPF3B), mRNA. /FEA=mRNA /GEN=UPF3B /PROD=similar to yeast Upf3, variant B /DB_XREF=gi:112711673 /UG=Hs.103832 similar to yeast Upf3, variant B /FI=gb:AY013251.1_gb:NM_023010.1
214030_at	Consensus includes gb:BE5013352 /FEA=EST /DB_XREF=gi:903760 /DB_XREF=est:7a4e05_x1 /CLONE=IMAGE:32223132 /UG=Hs.23294 ESTs, weakly similar to T15138 hypothetical protein T2882.4 - Caenorhabditis elegans
218073_s_at	gb:NM_017764.1 /DEF=Homo sapiens hypothetical protein FLJ20093 (FLJ20093), mRNA. /FEA=mRNA /GEN=FLJ20093 /PROD=hypothetical protein FLJ20093 /DB_XREF=gi:8923103 /UG=Hs.172572 hypothetical protein FLJ20093 /FI=gb:NM_017764.1
203466_s_at	Consensus includes gb:BE195973 /FEA=EST /DB_XREF=gi:11083411 /DB_XREF=est:7088c12_x1 /CLONE=IMAGE:36363391 /UG=Hs.102708 DKEFP43TA043 protein /FI=gb:NM_01536.1
219303_at	gb:NM_024546.1 /DEF=Homo sapiens hypothetical protein FLJ13449 (FLJ13449), mRNA. /FEA=mRNA /GEN=FLJ13449 /PROD=hypothetical protein FLJ13449 /FI=gb:NM_024546.1
202173_s_at	gb:NM_007146.1 /DEF=Homo sapiens zinc finger protein 61 (ZNF61), mRNA. /FEA=mRNA /GEN=ZNF61 /PROD=zinc finger protein 61 /DB_XREF=gi:911605967 /UG=Hs.6557 zinc finger protein 61 /FI=gb:D26118.1_gb:NM_007146.1
215903_s_at	Consensus includes gb:AK022697.1 /DEF=Homo sapiens zinc finger protein 61 /DB_XREF=gi:110430244 /UG=Hs.61629 calcium binding atopy-related autoantigen 1 related autoantigen CALC. /FEA=mRNA /DB_XREF=gi:110430244 /UG=Hs.61629 calcium binding atopy-related autoantigen 1
205842_s_at	gb:AF001362.1 /DEF=Homo sapiens Jak2 kinase (JAK2), mRNA, complete cds. /FEA=mRNA /GEN=JAK2 /PROD=Jak2 kinase /UG=Hs.11551 Janus kinase 2 (a protein tyrosine kinase) /FI=gb:NM_001972.2_gb:AE05216.1_gb:AF0593925.1_gb:AU011362.1
212702_s_at	Consensus includes gb:NM_045111 /FEA=EST /DB_XREF=gi:11862777 /DB_XREF=est:yz12f12_s1 /CLONE=IMAGE:2B2863 /UG=Hs.3303988 Homo sapiens, Similar to Bicaudal D (Drosophila) homolog 1, clone IMAGE:362454, mRNA, partial cds
201664_at	gb:AL136877.1 /DEF=Homo sapiens mRNA; cDNA DKFZp134E205 (from clone DKFZp134E205); complete cds. /FEA=mRNA /GEN=DKFZp134E205 /PROD=hypothetical protein /FI=gb:NM_005496.1_gb:AL136877.1
202060_at	gb:NM_014633.1 /DEF=Homo sapiens KIAA0155 gene product (KIAA0155), mRNA. /FEA=mRNA /GEN=KIAA0155 /PROD=KIAA0155 gene product /DB_XREF=gi:1661949 /UG=Hs.173288 KIAA0155 gene product /FI=gb:NM_014633.1_gb:D63875.1
203177_x_at	gb:NM_03201.1 /DEF=Homo sapiens transcription factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1), mRNA. /FEA=mRNA /GEN=TCF6L1 /PROD=transcription factor 6-like 1 (mitochondrial transcription factor 1-like) /FI=gb:M62810.1_gb:NM_003201.1

209748_at	gb:AB029006.1 /DEF=Homo sapiens mRNA for KIAA1083 protein, complete cds. /FEA=mRNA /GEN=KIAA1083 /PROD=KIAA1083 protein /DB_XREF=gi:5689502 /UG-Hs..6334 spastin, paraplegia 4 (autosomal dominant; spastin) /FI=gb:AB029006.1
200660_at	gb:NM_005620.1 /DEF=Homo sapiens S100 calcium-binding protein A11 /DB_XREF=gi:502056 /UG-Hs.256290 S100 calcium-binding protein A11 (calgizzarin) (S100A11), mRNA. /FEA=mRNA /GEN=mRNA /PROD=S100 calgizzarin protein /FI=gb:D30583.1
222119_s_at	Consensus includes gb:AU17620.1 /DEF=Homo sapiens mRNA, cDNA DKFZp564K2364 (from clone DKFZp564K2364); partial vitiligo-associated protein VIT-1. /GEN=DKFZp564K2364 /PROD=hypothetical protein /DB_XREF=gi:5912200 /UG-Hs.204289 vitiligo-associated protein VIT-1.
208334_s_at	gb:AF342815.1 /DEF=Homo sapiens colorectal carcinoma-derived galectin-8 variant I mRNA, complete cds. /FEA=mRNA /PROD=colorectal carcinoma-derived galectin-8 variant I /DB_XREF=gi:13249298 /UG-Hs.4082 lectin, galactoside-binding, soluble, 8 (galectin 8) /FI=gb:AF342815.1 gb:AF074000.1 /gb:NM_006499.1
211698_at	gb:AF342844.1 /DEF=Homo sapiens Rb- and p300-binding protein EID-1 mRNA, complete cds. /FEA=mRNA /PROD=Rb- and p300-binding protein EID-1 /DB_XREF=gi:13549113 /FI=gb:AF319444.1
212053_at	Consensus includes gb:AK025504.1 /DEF=Homo sapiens cDNA: FLJ21851 fis, clone HE01962. /FEA=mRNA /DB_XREF=gi:10438041 /UG-Hs.170218 KIAA0251 protein
209174_s_at	gb:BC009978.2 /DEF=Homo sapiens, hypothetical protein FLJ20259, clone MGC-5396, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein FLJ20259 /DB_XREF=gi:12803027 /UG-Hs.9556 hypothetical protein FLJ20259 /FI=gb:BC009978.2 gb:NM_017730.1
203476_at	gb:NM_006670.1 /DEF=Homo sapiens SVA oncofetal trophoblast glycoprotein (5T4), mRNA. /FEA=mRNA /GEN=5T4 /PROD=5T4 oncofetal trophoblast glycoprotein /FI=gb:NM_006670.1
203077_x_at	gb:AF077198.1 /DEF=Homo sapiens lysophospholipase mRNA, complete cds. /FEA=mRNA /PROD=lysophospholipase /DB_XREF=gi:1679009 /UG-Hs.125440
212721_at	Lysophospholipase I /FI=gb:AF01281.1 gb:AF077198.1 gb:NM_006330.1 gb:AF231053.1 Consensus includes gb:AI10380 /FEA=EST /DB_XREF=gi:5396946 /DB_XREF=est:wb87n10.x1 /CLONE=IMAGE:2312707 /UG-Hs.412724 Homo sapiens mRNA; CDS DKFZp564B176 (from clone DKFZp564B176)
218461_at	gb:NM_016301.1 /DEF=Homo sapiens protein x 0004 (LOC51184), mRNA. /FEA=mRNA /GEN=LOC51184 /PROD=protein x 0004 /DB_XREF=gi:9994188 protein x 0004 /FI=gb:AF117229.1 gb:NM_016301.1
214218_s_at	Consensus includes gb:AV699347 /FEA=EST /DB_XREF=gi:10301318 /DB_XREF=est:AV699347 /CLONE=GRCBPH07 /UG-Hs.83623 nuclear receptor subfamily 1 group I, member 3
218178_s_at	gb:NM_020412.1 /DEF=Homo sapiens CHMP1.5 protein (CHMP1..5), mRNA. /FEA=mRNA /GEN=CHMP1..5 /PROD=CHMP1..5 protein /DB_XREF=gi:9366900 /UG-Hs_42733
217851_s_at	CHMP1.5 protein /FI=gb:AF281064.1 gb:NM_020412.1 gb:NM_016015.1 /DEF=Homo sapiens CGF-107 protein (LOC51012), mRNA. /FEA=mRNA /GEN=LOC51012 /PROD=CGF-107 protein /DB_XREF=gi:7705609 /UG-Hs..3945 CGF-107 protein /FI=gb:AF151865.1 gb:NM_016045.1
203329_at	gb:NM_00333.1 /DEF=Homo sapiens c-src tyrosine kinase (CSK), mRNA. /FEA=mRNA /GEN=CSK /PROD=c-src tyrosine kinase /DB_XREF=gi:4758077 /UG-Hs..7793 c-src tyrosine kinase /FI=gb:NM_004383.1
203302_at	gb:NM_00788.1 /DEF=Homo sapiens deoxycytidine kinase (DCK), mRNA. /FEA=mRNA /GEN=DCK /PROD=deoxycytidine kinase /DB_XREF=gi:4503268 /UG-Hs..709 deoxycytidine kinase /FI=gb:M60527.1 gb:NM_00788.1
201949_x_at	Consensus includes gb:AU152341 /FEA=EST /DB_XREF=gi:12930514 /DB_XREF=est:AU152341 /CLONE=CSDOI07YCL3 (3 prime) /UG-Hs.76368 capping protein (actin filament) muscle Z-line, beta /FI=gb:NM_004930.1 gb:U03271.1
218096_at	gb:NM_018361.1 /DEF=Homo sapiens hypothetical protein FLJ11210, mRNA. /FEA=mRNA /GEN=FLJ11210 /PROD=hypothetical protein FLJ11210 /DB_XREF=gi:89229401 /UG-Hs.27842 hypothetical protein FLJ11210 /FI=gb:NM_018361.1
203255_at	gb:NM_018653.1 /DEF=Homo sapiens vitiligo-associated protein VIT-1 (VIT1), mRNA. /FEA=mRNA /GEN=VIT1 /PROD=vitiligo-associated protein VIT-1 /DB_XREF=gi:10048403 /UG-Hs..284289 vitiligo-associated protein VIT-1 /FI=gb:NM_018693.1 gb:AE264714.1
203855_at	gb:NM_014959.1 /DEF=Homo sapiens KIAA0893 protein (KIAA0893), mRNA. /FEA=mRNA /GEN=KIAA0893 /PROD=KIAA0893 protein /DB_XREF=gi:7662363 /UG-Hs..3830 KIAA0893 protein /FI=gb:AB020700.1 gb:NM_014969.1
218846_at	gb:NM_004830.1 /DEF=Homo sapiens cofactor required for Spi transcriptional activation, subunit 3 (130kD) (CSP3), mRNA. /FEA=mRNA /GEN=CRSP /PROD=cofactor required for Spi transcriptional activation, subunit 3 (130kD) /DB_XREF=gi:7019352 /UG-Hs.29679 cofactor required for Spi transcriptional activation, subunit 3 (130kD) /FI=gb:AF135022.1 gb:NM_004830.1
208988_at	Consensus includes gb:BE675843 /FEA=EST /DB_XREF=gi:10036384 /DB_XREF=est:7E17b04.x1 /CLONE=IMAGE:3294895 /UG-Hs.219614 f-box and leucine-rich repeat protein 11 /FI=gb:AF119221.1
216202_s_at	Consensus includes gb:U15555.1 /DEF=Human serine palmitoyltransferase (UCB2) mRNA, partial cds. /FEA=mRNA /GEN=UCB2 /PROD=serine palmitoyltransferase /DB_XREF=gi:10015944 /UG-Hs..59403 serine palmitoyltransferase, long chain base subunit 2
216954_x_at	Consensus includes gb:S777556.1 /DEF=Homo sapiens oligomycin sensitivity conferral protein ocp-like protein mRNA, partial cds. /FEA=mRNA /

212753_at	PROD=oligomycin sensitivity conferring protein /DB_XREF=q1:944964 /UG=Hs.76572 ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) Consensus includes gb:AI592203 /DB_XREF=q1:4969843 /DB_XREF=est:wdd7h12.x1 /CLONE=IMAGE:2330375 /UG=Hs.8834 ring finger protein 3
207691_x_at	gb:NM_001776.1 /DEF=Homo sapiens ectonucleoside triphosphate diphosphohydrolase 1 (ENTPD1), mRNA. /FEA=mRNA /GEN=ENTPD1 /PROD=ectonucleoside triphosphate diphosphohydrolase 1
209967_at	gb:NM_000942.1 /DEF=Homo sapiens Peptidyl-prolyl isomerase B (cyclophilin B) (PPIB), mRNA. /FEA=mRNA /GEN=PPIB /PROD=peptidylprolyl isomerase B (cyclophilin B) /DB_XREF=q1:4758949 /UG=Hs.699 peptidylprolyl isomerase B (cyclophilin B) /FI=gb:BC001125.1 qb:M60857.1
201988_s_at	gb:NM_063573.1 qb:NM_00942.1 Consensus includes gb:BF438056 /FEA=EST /DB_XREF=q1:11450573 /DB_XREF=est:7q6e01.x1 /CLONE=IMAGE:3703369 /UG=Hs.13313 cAMP responsive element binding protein-like 2 /FL=gb:AF039081.1 qb:NM_001310.1
202142_at	gb:BC0005090.1 /DEF=Homo sapiens, COP9 homolog, clone MGC:1297, mRNA, complete cds. /FEA=mRNA /PROD=COP9 homolog /DB_XREF=q1:13111846 /UG=Hs.75193 COP9 homolog /FL=gb:BC0005090.1 qb:NM_006710.1
218238_at	gb:NM_012341.1 /DEF=Homo sapiens GTP-binding protein (NEF), mRNA. /FEA=mRNA /GEN=NGB /PROD=GTP-binding protein /DB_XREF=q1:6912531 /UG=Hs.215166 GTP-binding protein /FI=gb:AF323535.1 qb:NM_012341.1
205552_s_at	gb:NM_002534.1 /DEF=Homo sapiens 2',5'-oligoadenylate synthetase 1 (40-46 kD) (OAS1), transcript variant E16, mRNA. /FEA=mRNA /GEN=OAS1 /PROD=2',5'-oligoadenylate synthetase 1, isoform E16 /DB_XREF=q1:8051622 /UG=Hs.82396 2',5'-oligoadenylate synthetase 1 (40-46 kD) /FI=gb:BC0010562.1
202541_at	gb:NM_000668.1 qb:NM_002534.1 Consensus includes gb:BF389679 /FEA=EST /DB_XREF=q1:11682003 /DB_XREF=est:na08805.x1 /CLONE=IMAGE:3253977 /UG=Hs.146401 small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating protein) /FI=gb:NM_004757.1 qb:U1017.1
221699_s_at	gb:AF334103.1 /DEF=Homo sapiens nucleolar protein GU2 mRNA, complete cds. /FEA=mRNA /PROD=nucleolar protein GU2 /DB_XREF=q1:13540303 /FI=gb:AF334103.1
202090_s_at	gb:NM_006830.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase (6.4kD) subunit /DB_XREF=q1:5803216 /DB_XREF=q1:5803216 /UG=Hs.8372 ubiquinol-cytochrome c reductase (6.4kD) subunit /PROD=ubiquinol-cytochrome c reductase (6.4kD) subunit /EL=gb:D5536.1 qb:NM_006830.1
202382_s_at	gb:NM_005471.1 /DEF=Homo sapiens glucosamine-6-phosphate isomerase (GNPI), mRNA. /FEA=mRNA /GEN=GNPI /PROD=glucosamine-6-phosphate isomerase /DB_XREF=q1:13027377 /UG=Hs.278500 glucosamine-6-phosphate isomerase (GNPI), mRNA. /FEA=mRNA /GEN=GNPI /PROD=glucosamine-6-phosphate isomerase
220408_x_at	gb:NM_017569.1 /DEF=Homo sapiens transcription factor (P38 interacting protein) (P38IP), mRNA. /FEA=mRNA /GEN=P38IP /PROD=transcription factor (P38 interacting protein) /FI=gb:AF093250.1
208264_s_at	gb:NM_007569.1 /PROD=eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD) (EIF3S1), mRNA. /FEA=mRNA /GEN=EIF3S1 /PROD=eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD) /FI=gb:U97670.1 qb:NM_003158.1
202872_at	Consensus includes gb:AW24925 /FEA=EST /DB_XREF=q1:5878455 /DB_XREF=est:Wd92q09.x1 /CLONE=IMAGE:2327552 /UG=Hs.86305 ATPase, H+ transport-ing, lysosomal (vacuolar proton pump) 42kD /FI=gb:NM_001695.1
214835_s_at	gb:AF131748.1 /DEF=Homo sapiens clone 25191 GTP-specific succinyl-CoA synthetase beta subunit /DB_XREF=q1:4406553 /UG=Hs.247309 succinate-CoA ligase, ssp-forming, beta subunit Consensus includes gb:AF100338.1 qb:NM_003921.1 /DB_XREF=q1:4092066 /UG=Hs.193516 B-cell CLLymphoma 10 /FI=gb:AF082283.1
205263_at	gb:AF082283.1 /PROD=card-containing poppetic signaling protein (BCJ10), mRNA, complete cds. /FEA=mRNA /GEN=BCJ10 /PROD=card-containing poppetic signaling protein (BCJ10) mRNA, complete cds. /FEA=mRNA /GEN=BCJ10 /FI=gb:AF127386.1 qb:AF134395.1 qb:AE105066.1
218512_at	gb:NM_019256.1 /DEF=Homo sapiens hypothetical protein ELJ10881 (ELJ10881), mRNA. /FEA=mRNA /GEN=ELJ10881 /PROD=hypothetical protein ELJ10881 /DB_XREF=q1:8922736 /UG=Hs.73291 hypothetical protein ELJ10881 /FI=gb:AF212546.1 qb:NM_019256.1
210283_x_at	gb:BC005295.1 /DEF=Homo sapiens, similar to polyadenylate binding protein-1, clone MGC:123160, mRNA, complete cds. /FEA=mRNA /PROD=similar to polyadenylate binding protein-1 /FI=gb:BC005295.1
202724_s_at	gb:NM_002015.2 /DEF=Homo sapiens forkhead box O1A (rhabdomyosarcoma) (FOXO1A), mRNA. /FEA=mRNA /GEN=FOXO1A /PROD=forkhead box O1A /DB_XREF=q1:9557221 /UG=Hs.170133 forkhead box O1A (rhabdomyosarcoma) /FI=gb:AF032885.1 qb:U02310.1 qb:NM_002015.2
212058_at	Consensus includes gb:AI184562 /FEA=EST /DB_XREF=q1:3733200 /DB_XREF=est:qd00605.x1 /CLONE=IMAGE:1733841 /UG=Hs.7976 KIAA0332 protein

21200_6_at	Consensus includes gb:AU149908 / FEA=EST / DB_XREF=gi:110111429 / DB_XREF=est:AU149908 / CLONE=NT2RP2000896 / UG=Hs .77495 UBX domain-containing 1
22204_0_at	Consensus includes gb:AU144007 / FEA=EST / DB_XREF=gi:3565816 / DB_XREF=est:gb33c06.x1 / CLONE=IMAGE:1698058 / UG=Hs .249495
20237_3_s_at	gb:AF55648.1 / DEF=Homo sapiens ribonucleaseprotein A1 heterogenous nuclear ribonucleoprotein Al GTPase-activating protein, non-catalytic subunit (150kD) / EL=gb:AF004828.1 qb:NM_012414.1
209301_1_at	gb:NM_036532.1 / DEF=Human carbonic anhydrase III mRNA, complete cds. / FEA=mRNA / GEN=CA2 / DB_XREF=gi:1179794 / UG=Hs .155097 carbonic anhydrase II / EL=gb:AF030371.1 qb:NM_000067.1
213264_at	Consensus includes gb:AW025150 / FEA=EST / DB_XREF=gi:5878680 / DB_XREF=est:wo94e06.x1 / CLONE=IMAGE:2527714 / UG=Hs .211601 mitogen-activated protein kinase kinase kinase 12
20286_3_at	gb:NM_003113.1 / DEF=Homo sapiens nuclear antigen Sp100 (SP100), mRNA. / FEA=mRNA / GEN=SP100 / PROD=nuclear antigen Sp100 / DB_XREF=gi:4507164 / UG=Hs .77617 nuclear antigen Sp100 / EL=gb:NM00618.1 qb:NM_003113.1
217679_x_at	Consensus includes gb:AU1683552 / FEA=EST / DB_XREF=gi:4893734 / DB_XREF=est:tm67hn02.x1 / CLONE=IMAGE:2274675 / UG=Hs .201605 ESTs, Moderately similar to ALU8 HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H. sapiens
212802_s_at	Consensus includes gb:AK023841.1 / DEF=Homo sapiens cDNA FLJ13779 fis, clone PLACE4000445, highly similar to Homo sapiens mRNA; cDNA DKFZp43C212 (from clone DKFZp43C212). / FEA=mRNA / DB_XREF=gi:10435900 / UG=Hs .172069 DKFZp43C212 protein
21034_6_s_at	gb:AF21224.1 / DEF=Homo sapiens CLK4 mRNA, complete cds. / FEA=mRNA / PROD=CLK4 / DB_XREF=gi:9437514 / UG=Hs .295231 Homo sapiens CLK4 mRNA, complete cds / EL=gb:AF21224.1
208848_at	gb:NM_03041.1 / DEF=Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds. / FEA=mRNA / GEN=ADH5 / PROD=alcohol dehydrogenase 3 /
221978_at	Consensus includes gb:BE136825 / FEA=EST / DB_XREF=gi:8001325 / DB_XREF=est:xw96a07.x1 / CLONE=IMAGE:2835828 / UG=Hs .110309 major histocompatibility complex, class I, F
217526_at	Consensus includes gb:AU1478300 / FEA=EST / DB_XREF=gi:4371526 / DB_XREF=est:km39e01.x1 / CLONE=IMAGE:2160504 / UG=Hs .192789 ESTs, weakly similar to ALU6 HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY H. sapiens
218322_s_at	gb:NM_016234.2 / DEF=Homo sapiens long-chain fatty acid coenzyme A ligase 5 (FACL5), mRNA. / FEA=mRNA / GEN=FACL5 / PROD=long-chain fatty acid coenzyme A ligase 5 / EL=gb:NM_016234.2 qb:AB033889.1
212513_at	Consensus includes gb:AU1991252 / FEA=EST / DB_XREF=gi:5638157 / DB_XREF=est:wu41e09.x1 / CLONE=IMAGE:2522632 / UG=Hs .87497 butyrophilin, subfamily 3, member A2
204566_at	gb:NM_003620.1 / DEF=Homo sapiens protein phosphatase 1D magnesium-dependent, delta isoform / DB_XREF=gi:4505996 / UG=Hs .100980 protein phosphatase 1D magnesium-dependent, delta isoform / EL=gb:U78305.1 qb:NM_003620.1

Tabelle 6: Gene aus Clusteranalyse 6

Affymetrix- interne Be- zeichnung	Beschreibung der Sequenz in der Genbank Datenbank
202018_s_at	gb;NM_002343.1 /DEF=Homo sapiens lactotransferrin (LTF), mRNA. /FEA=mRNA /GEN=LTF /PROD=lactotransferrin /DB_XREF=gi:4505042 /UG-Hs_105938_lactotransferrin /FL=gb;AF33168.1 gb;NM3202.1 qb;NN 003343.1
216379_x_at	Consensus includes qb;AK00168.1 /DEF=Homo sapiens CD24 signal transducer mRNA. /FEA=mRNA /DB_XREF=gi:7020079 /UG-Hs_332045 Homo sapiens cDNA FLJ20161 fis, Clone COL0952, highly similar to L33930
209771_x_at	Homo sapiens CD24 signal transducer mRNA. /FEA=mRNA /DB_XREF=gi:7020079 /UG-Hs_332045 Homo sapiens cDNA FLJ20161 fis, Clone COL0952, highly similar to L33930
206676_at	Consensus includes qb;RA761181 /DEF=EST /DB_XREF=est:rz09q03.s1 /CLONE=IMAGE:1287316 /UG-Hs_286124_CD24_antigen /small cell lung carcinoma cluster 4 antigen/ /FL=gb;X69397.1 /FEA=mRNA /GEN=NCA /PROD=non-specific cross-reacting antigen (NCA) mRNA, complete cds.
210254_at	gb;NM33326.1 /DEF=Human nonspecific cross-reacting antigen molecule 8 /FL=gb;M33326.1 qb;NN 001816.1 /UG-Hs_411 carcinoembryonic antigen-related cell adhesion molecule 8 /FL=gb;M33326.1 qb;NN 001816.1 /DEF=Homo sapiens IgE receptor beta chain (HITm4) mRNA, complete cds. /FEA=mRNA /GEN=HITm4 /PROD=IgE receptor beta subunit /DB_XREF=gi:561638 /UG-Hs_99960 membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific) /FL=gb;NM_000538.1 qb;I55848.1
203887_s_at	gb;NM_000361.1 /DEF=Homo sapiens thrombomodulin (TMBD), mRNA. /FEA=mRNA /GEN=TMBD /PROD=thrombomodulin /DB_XREF=gi:4507482 /UG-Hs_2030 thrombomodulin /FL=gb;M16552.1 qb;NN 000361.1
212768_s_at	Consensus includes qb;AL390736 /DEF=Human DNA sequence from clone RP11-20B19 on chromosome 13 Contains ESTs, STSs and GSSs. Contains the gene for the GM112 protein with two isoforms (GM112 and KIAA294) /FEA=mRNA /DB_XREF=gi:11182238 /UG-Hs_273321 differentially expressed in hematopoietic lineages
202887_s_at	gb;NM_019056.1 /DEF=Homo sapiens hypothetical protein (FLJ20500), mRNA. /FEA=mRNA /GEN=FLJ20500 /PROD=hypothetical protein /DB_XREF=gi:9506686 /UG-Hs_111244 hypothetical protein /FL=gb;AL136668.1 qb;NN 019058.1
200916_at	gb;NM_003564.1 /DEF=Homo sapiens transgelin 2 (TAGLN2), mRNA. /FEA=mRNA /GEN=TAGLN2 /PROD=transgelin 2 /DB_XREF=gi:4507356 /UG-Hs_75725 transgelin 2 /FL=gb;D21261.1 qb;NM_003564.1
206157_at	gb;NM_002852.1 /DEF=Homo sapiens pentaxin-related gene, rapidly induced by IL-1 beta /DB_XREF=gi:4506332 /UG-Hs_2050 pentaxin-related gene, rapidly induced by IL-1 beta /FL=gb;M31166.1 qb;NN 002852.1
209369_at	gb;NM_63310.1 /DEF=Human 1,2-cyclic-inositol-phosphodiesterase (ANX3) mRNA, complete cds. /FEA=mRNA /GEN=ANX3 /PROD=1,2-cyclic-inositol-phosphodiesterase /DB_XREF=gi:178656 /UG-Hs_1378 annexin A3 /FL=gb;BC000871.1
202497_x_at	Consensus includes qb;AL631159 /DEF=EST /DB_XREF=est:ts93d05.x1 /CLONE=IMAGE:2238825 /UG-Hs_7594 solute carrier family 2 (facilitated glucose transporter), member 3 /FL=gb;M20681.1 qb;NN 006931.1
205513_at	gb;NM_001062.1 /DEF=Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) /DB_XREF=gi:4507406 /UG-Hs_2012 transcobalamin I (vitamin B12 binding protein, R binder family) /FL=gb;J05068.1 qb;NN 001062.1
206697_s_at	gb;NM_005143.1 /DEF=Homo sapiens haptoglobin (HP), mRNA. /FEA=mRNA /GEN=HP /PROD=haptoglobin /DB_XREF=gi:4826761 /UG-Hs_75990 haptoglobin /FL=gb;K000422.1 qb;NN 005143.1
202146_at	Consensus includes qb;RA741426 /DEF=EST /DB_XREF=est:nx88e08.s1 /CLONE=IMAGE:126350 /UG-Hs_7879 interferon-related developmental regulator 1 /FL=gb;186001272.1 qb;NN 001550.1
266_s_at	L33930 /FEATURE=/DEFINITION=HMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3 region
211657_at	gb;NM_018728.1 /DEF=Human nonspecific cross-reacting antigen mRNA, complete cds. /FEA=mRNA /GEN=NCA; NCA /PROD=non-specific cross-reacting antigen /DB_XREF=gi:189084 /FL=gb;M18728.1
205214_at	gb;NM_004226.1 /DEF=Homo sapiens serinethreonine kinase 17b (apoptosis-inducing) (STK17B), mRNA. /FEA=mRNA /GEN=STK17B /PROD=serinethreonine kinase 17b (apoptosis-inducing) /DB_XREF=gi:4758193 /UG-Hs_120996 serinethreonine kinase 17b

(apoptosis-inducing) /FL=gb:AB011421.1 qb:NM_004226.1	qb:NM_015675.1 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA. /FEA=mRNA /GEN=GADD45B /PROD=DKEZP56GB133 protein /DB_XREF=gi:9945331 /UG-Hs:110571 growth arrest and DNA-damage-inducible, beta /FL=gb:AF0950.1
206341_s_at	qb:NM_013959.1 /DEF=Homo sapiens neuregulin 1 (NRG1), transcript variant Smnf, mRNA. /FEA=mRNA /GEN=NRG1 /PROD=neuregulin 1 isoform Smnf /DB_XREF=gi:7669517 /UG-Hs:172816 neuregulin 1 /FL=gb:NM_013959.1 qb:141827.1
214146_s_at	Consensus includes qb:RG6130 /FEA=EST /DB_XREF=gi:836009 /DB_XREF=est:V118N03.S1 /CLONE=IMAGE:139637 /UG-Hs:2164 pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide 2)
215716_s_at	Consensus includes qb:Li4561 /DEF=Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds /FEA=mRNA 2 /DB_XREF=gi:4165324 /OC-Hs:78546 ATPase, Ca++ transporting, plasma membrane 1
201179_s_at	gb:J03005.1 /DEF=Human alternative guanine nucleotide-binding regulatory protein (G alpha-inhibitory-subunit mRNA, complete cds, /FEA=mRNA /GEN=GNAL1 /DB_XREF=gi:183183 /UG-Hs:37399 guanine nucleotide binding protein (G Protein), alpha inhibiting activity polypeptide 3 /FL=gb:J03005.1 qb:J03198.1 qb:M2743.1 qb:J03238.1 qb:NM_006456.1
201626_at	Consensus includes qb:BG292233 /FEA=EST /DB_XREF=gi:13050848 /DB_XREF=est:602386668FB1 /CLONE=IMAGE:055342.1
209728_at	qb:EC005312.1 /DEF=Homo sapiens, clone MGC:12387, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:12387) /UG-Hs:12813 DKEZP430J214 protein
212665_at	Consensus includes qb:AL556338 /FEA=EST /DB_XREF=gi:12859113 /DB_XREF=est:AL556438 /CLONE=CS0DR0047118 (3 prime) /GEN=SPARC /PROD=secreted protein, acidic, cysteine-rich (osteonectin) (SPARC), mRNA. /FEA=mRNA /cysteine-rich (osteonectin) /FL=gb:EC004974.1 qb:NM_003118.1
201407_s_at	Consensus includes qb:AU18672 /FEA=EST /DB_XREF=est:982501.x1 /CLONE=IMAGE:1745497 /UG-Hs:21537 protein phosphatase 1, catalytic subunit, beta isoform /FL=gb:NM_002709.1 qb:AU029205.1
203505_at	qb:AF285167.1 /DEF=Homo sapiens ATP-binding cassette transporter 1 (ABC1) mRNA, complete cds. /FEA=mRNA /GEN=ABC1 /PROD=ATP-binding cassette transporter 1 /DB_XREF=gi:9755158 /UG-Hs:211562 ATP-binding cassette, sub-family A (ABC1), member 1 /FL=gb:AF16281.1 qb:NM_005502.1 qb:AEF285167.1
221802_s_at	Consensus includes qb:AU157109 /FEA=EST /DB_XREF=gi:111018630 /DB_XREF=est:AU157109 /CLONE=PLACT006159 /UG-Hs:23740 KIAA1598 protein
201844_s_at	Consensus includes qb:W34482 /FEA=EST /DB_XREF=gi:1395613 /DB_XREF=est:zdb89h07.s1 /CLONE=IMAGE:356701 /UG-Hs:1910 RING1 and YY1 binding protein /FL=gb:AB179286.1 /DB_XREF=gi:1269908
2063390_x_at	qb:NM_002619.1 /DEF=Homo sapiens platelet factor 4 (PFA), mRNA. /FEA=mRNA /GEN=PFA /PROD=platelet factor 4 /DB_XREF=gi:4505732 /UG-Hs:81564 platelet factor 4 /FL=gb:M25891.1 qb:NM_002619.1
212569_at	Consensus includes qb:AV699744 /FEA=EST /DB_XREF=gi:10301715 /DB_XREF=est:AV699744 /CLONE=SKCEF05 /UG-Hs:8118 KIAA0650 protein
211960_s_at	Consensus includes qb:BG261116 /FEA=EST /DB_XREF=gi:127171232 /DB_XREF=est:60237192F1 /CLONE=IMAGE:41484422 /UG-Hs:237955 hypothetical protein PRO2706
202422_s_at	qb:NM_022977.1 /DEF=Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (EPLC4), transcript variant 2, mRNA. /FEA=mRNA /GEN=EPLC4 /PROD=long-chain fatty-acid-Coenzyme A ligase 4 isoform 2 /DB_XREF=gi:1269908
221958_s_at	Consensus includes qb:AA175681 /FEA=EST /DB_XREF=gi:2835015 /DB_XREF=est:Z331a02.s1 /CLONE=IMAGE:378506 /UG-Hs:250746 hypothetical protein FLJ23091
204621_s_at	Consensus includes qb:AJ935096 /FEA=EST /DB_XREF=gi:5673966 /DB_XREF=est:WP13e10.x1 /CLONE=IMAGE:2464746 /UG-Hs:32120 nuclear receptor subfamily 4, group A, member 2 /FL=gb:NM_006186.1
201409_s_at	qb:NM_002709.1 /DEF=Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PP1CB), mRNA. /FEA=mRNA /GEN=PP1CB /PROD=protein phosphatase 1, catalytic subunit, betaisotform /DB_XREF=gi:4506004 /UG-Hs:21537 protein phosphatase 1, catalytic subunit, beta isoform /FL=gb:NM_002709.1 qb:AEF032905.1
201662_s_at	qb:DB9053.1 /DEF=Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds. /FEA=mRNA /PROD=Acyl-CoA synthetase 3 /DB_XREF=gi:4165017 /UG-Hs:268012 fatty-acid-Coenzyme A ligase, long-chain 3 /FL=gb:NM_004457.2 qb:D88053.1 qb:AEF116690.1
220987_s_at	qb:NM_03952.1 /DEF=Homo sapiens hypothetical protein DKEZP434J037 (DKEZP434J037) mRNA. /FEA=mRNA /GEN=DKEZP434J037 /PROD=hypothetical protein DKEZP434J037 /FL=gb:NM_03952.1

21219607_s_at	Sub:NM_024021.1 / DEF=homo sapiens membrane-spanning 4-domains, subfamily A, member 4 (MS4A4), mRNA. /FEA=mRNA /GEN=MS4A4 /PROD=membrane-spanning 4-domains, subfamily A, member 4 /DB_XREF=gi:NM_016650.1 /UG-Hs:325960 membrane-spanning 4-domains, subfamily A, member 4 /FL-gb:AB013102.1 b:NM_024021.1 qb:NM_016650.1 /
201565_s_at	Sub:NM_002166.1 / DEF=homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA. /GEN=ID2 /PROD=inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /DB_XREF=gi:1504570 /UG-Hs:180919 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /FL_qb:n97796.1 qb:NM_002166.1 qb:D13891.1
21213327_s_at	Consensus includes: gba:PAI20101 /BEA=EST /DB_XREF=gi:5439180 /DB_XREF=est:wg56612.x1 (CLONE=IMAGE:2369111 /UG-Hs:42400 ubiquitin specific protease 12 Sub:NM_017495.1 /DBE=homo sapiens zinc finger homeobox 1B (ZFPK1B), mRNA. /FEA=mRNA /GEN=ZFPK1B /PROD=zinc finger homeobox 1B /DB_XREF=gi:17662183 /UG-Hs:34817 zinc finger homeobox 1B /FL_qb:AB011141.1 qb:NM_014795.1 /
20203603_s_at	Sub:NM_01380.1 /DBE=homo sapiens p75NTR-associated cell death executor; ovarian granulosa cell protein (13kd) (DXS694E), mRNA. /FEA=mRNA /GEN=DXS694E /PROD=p75NTR-associated cell death executor; ovarian granulosa cell protein (13kd) /DB_XREF=gi:7657043 /UG-Hs:17775 p75NTR-associated cell death executor; ovarian granulosa cell protein (13kd) /EL_qb:NM_014380.1 qb:AF187064.1
20206710_s_at	Sub:NM_012307.1 /DEF=homo sapiens differentially expressed in adenocarcinoma of the lung (KIAA0987), mRNA. /FEA=mRNA /GEN=KIAA0987 /PROD=differentially expressed in adenocarcinoma of the lung (KIAA0987) /UG-Hs:103829 extracellular membrane protein band 4.1-like 3 (EFEMP3) /DB_XREF=gi:HE63072.1 qb:NM_012307.1
20204342_BT	Sub:NM_013386.1 /DBE=homo sapiens hypothetical protein (DKF2P386GG0123), mRNA. /FEA=mRNA /GEN=DKF2P386GG0123 /PROD=hypothetical protein /EI_qb:AL050209.1 qb:NM_013386.1
20204393_s_at	Sub:NM_001099.2 /DBE=homo sapiens acid phosphatase, prostate (ACPP), mRNA. /FEA=mRNA /GEN=ACPP /PROD=acid phosphatase precursor /DB_XREF=gi:6382063 /UG-Hs:1832 acid phosphatase, prostate /FL_qb:MA4902.1 qb:MA4840.1 qb:NM_001099.2
20200719_at	Consensus includes: gba:BE36403 /BEA=EST /DB_XREF=gi:11767371 /DB_XREF=est:601657616R1 (CLONE=IMAGE:38785955 /UG-Hs:17166 transcription elongation factor B (SII), polypeptide 1-like /FL_qb:NM_003197.2 /
20202731_at	Sub:NM_014456.1 /DBE=homo sapiens programmed cell death 4 (PCD4), mRNA. /FEA=mRNA /GEN=PCD4 /PROD=programmed cell death 4 /DB_XREF=gi:7657448 /UG-Hs:296251 programmed cell death 4 /FL_qb:gb:966638.1 qb:NM_014456.1
20204094_s_at	Sub:NM_014779.1 /DBE=homo sapiens KIAA0669 gene product (KIAA0669), mRNA. /FEA=mRNA /GEN=KIAA0669 /PROD=KIAA0669 gene product /DB_XREF=gi:17662235 /UG-Hs:52226 KIAA0669 gene product /FL_qb:AB014569.1 qb:NM_014797.1 /FEA=mRNA /PROD=Similar to LIM protein, clone MG-5344, mRNA, complete cds. /DB_XREF=gi:12654194 /UG-Hs:75807 PDZ and LIN domain 1 (elffin), /FL_qb:BC000915.1
20088690_s_at	Sub:NM_0128158.1 /DBE=homo sapiens nuclear receptor coactivator RAP250 mRNA, complete cds. /FEA=mRNA /PROD=nuclear receptor coactivator RAP250 mRNA, complete cds. /FL_qb:AB014567.3 /UG-Hs:159613 thyroid hormone receptor binding protein /FL_qb:AB17388.1 qb:NM_0128158.1 qb:NM_014071.3 qb:AF245115.1
2008979_at	Sub:NM_015878.1 /DBE=homo sapiens antizyme inhibitor (LOC51582), mRNA. /FEA=mRNA /GEN=LOC51582 /PROD=antizyme inhibitor /DB_XREF=gi:770621.9 /UG-Hs:223014 antizyme inhibitor /FL_qb:DB88674.1 qb:NM_015878.1
20201345_s_at	Sub:NM_003339.1 /DBE=homo sapiens ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) /FEA=mRNA /GEN=DEB2D2 /PROD=ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) /DB_XREF=gi:1507774 /UG-Hs:1083332 ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) /FL_qb:gb:1039317.1 qb:NM_003339.1
20201772_at	Sub:NM_003266.1 /DBE=homo sapiens toll-like receptor 4 (TLR4), mRNA. /FEA=mRNA /GEN=TLR4 /PROT=toll-like receptor 4 /DB_XREF=gi:1507332 /UG-Hs:159239 toll-like receptor 4 /FL_qb:gb:U88880.1 qb:NM_003266.1
20208878_s_at	Sub:AF092132.1 /DBE=homo sapiens PAK2 mRNA, complete cds. /FEA=mRNA /PROD=PAK2 /DB_XREF=gi:51138913 /UG-Hs:284275 Homo sapiens PAK2 mRNA, 7 complete cds /FL_qb:AF092132.1
21212628_at	Consensus includes: gba:BG292065 /FEA=EST /DB_XREF=gi:13050507 /DB_XREF=est:602386350F1 /CLONE=IMAGE:4515036 /UG-Hs:69171 protein kinase C-like 2
21212928_at	Consensus includes: gba:AF050331 /DEF=Human DNA sequence from clone 48613 on chromosome 6q22.1-22.3. Contains the part of a gene for a novel protein, the gene for KIAA0721 (NAP (Nucleosome Assembly Protein) domain containing protein), the TSPY gene (testis specific protein... /FEA=mRNA /PROD=PRO0189
22221060_s_at	Sub:NM_003266.1 /DBE=homo sapiens toll-like receptor 4 (TLR4), mRNA. /FEA=mRNA /GEN=TLR4 /PROT=toll-like receptor 4 /DB_XREF=gi:1507332 /UG-Hs:284141 KIAA0721 protein /FL_qb:NM_021549.1 /DB_XREF=gi:5668655 /UG-Hs:284141 KIAA0721 protein /FL_qb:NM_021549.1
2221569_s_at	Sub:AF090300.1 /DBE=homo sapiens clone H00189 PRO0189 mRNA, complete cds. /FEA=mRNA /GEN=PRO0189 /DB_XREF=gi:6690176 /UG-Hs:91393 Homo sapiens cDNA: FLJ21887 firs, clone HE03135, highly similar to AF090900 Homo sapiens clone H00189 PRO0189 mRNA /FL_qb:AF090900.1
20201408_at	Consensus includes: gba:W67887 /FEA=EST /DB_XREF=gi:13176776 /DB_XREF=est:z338c1.81 /CLONE=IMAGE:312932 /UG-Hs:21537 protein phosphatase 1, catalytic subunit, beta isoform /FL_qb:NM_002709.1 qb:AF092950.1

202270_at	gb:NM_002053.1 /DEF=Homo sapiens guanylate binding protein 1, interferon-inducible, 67kd (GDPB1), mRNA. /FEA=mRNA /GEN=gb:NM_002053.1 /gb:NM_62561 guanylate binding protein 1, interferon-inducible, 67kd /EI=gb:BC002666.1 qb:NM_002053.1.
202605_s_at	gb:NM_012290.1 /DEF=Homo sapiens tousled-like kinase 1 (TLK1), mRNA. /FEA=mRNA /GEN=TLK1 /PROD=tousled-like kinase 1 /DB_XREF=gi:6912719 /UG=Hs.18895 tousled-like kinase 1 /EI=gb:AB004685.1 qb:NM_012290.1 qb:AF46219.1
216037_x_at	Consensus includes gb:AA64011 /DB_XREF=est:ac03f10.s1 /CLONE=IMAGE:855403 /UG=Hs.113638 transcription factor 7- like 2 (T-cell specific, HMG-box)
221561_at	gb:L21934.2 /DEF=Homo sapiens acyl-coenzyme A: cholesterol acyltransferase mRNA, complete cds. /FEA=mRNA /PROD=acyl-coenzyme A: cholesterol acyltransferase /DB_XREF=gi:4878021 /UG=Hs.14553 sterol acyltransferase (acyl-coenzyme A: cholesterol acyltransferase) 1 /EI=gb:NM_003101.1 qb:L21934.2
203680_at	gb:NM_002736.1 /DEF=Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA. /FEA=mRNA /GEN=PRKAR2B /PROD=protein kinase, cAMP-dependent, regulatory, type II, beta /DB_XREF=gi:506064 /UG=Hs.7439 protein kinase, cAMP-dependent, regulatory, type II, beta /EI=gb:NM_01158.1 qb:NM_002736.1
215111_s_at	Consensus includes gb:AK027071.1 /DEF=Homo sapiens tSC-22 protein mRNA. /FEA=mRNA /DB_XREF=est:gi:10140100 /UG=Hs.144360 transforming growth factor beta-stimulated protein TSC-22
202211_at	gb:BC005122.1 /DEF=Homo sapiens ADP-ribosylation factor GTPase activating protein 1, clone MGC:10272, mRNA, complete cds. /FEA=mRNA /PROD=ADP-ribosylation factor GTPase activating protein 1 /EI=gb:BC005122.1 qb:AB11847.1 qb:NM_01450.1
221918_at	Consensus includes gb:AIT42210 /FEA=EST /DB_XREF=est:wg39c02.x1 /CLONE=IMAGE:2367158 /UG=Hs.183302 ESTs
213251_at	Consensus includes gb:AV712064 /FEA=EST /DB_XREF=est:AV712064 /CLONE=DCAUD05 /UG=Hs.9456 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
209186_at	gb:NM_23114.1 /DEF=Homo sapiens calcium-ATPase (Hk1), mRNA, complete cds. /FEA=mRNA /GEN=HK1 /DB_XREF=gi:184100 /UG=Hs.1526 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 /EI=gb:NM_23114.1
210996_s_at	gb:U03430.1 /DEF=Human epsilon isoform 14-3-3 protein mRNA, complete cds. /FEA=mRNA /PROD=14-3-3 protein /DB_XREF=gi:1096984 /UG=Hs.79474 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide /EI=gb:U43399.1 qb:U4340.1
213621_at	Consensus includes gb:AR873600 /FEA=EST /DB_XREF=est:ch12a02.s1 /CLONE=IMAGE:1323434 /UG=Hs.42245 acid sphingomyelinase-like phosphodiesterase
204634_at	gb:NM_00157.1 /DEF=Homo sapiens serinethreonine kinase 2 (STK2), mRNA. /FEA=mRNA /GEN=STK2 /PROD=serinethreonine kinase 2 /DB_XREF=gi:450276 /UG=Hs.1057 serinethreonine kinase 2 /EI=gb:L20321.1 qb:NM_003157.1
212515_s_at	Consensus includes gb:BG492502 /FEA=EST /DB_XREF=gi:13454114 /DB_XREF=est:602536566F1 /CLONE=IMAGE:4652296 /UG=Hs.147916 DEADRH (Asp-Glu-Ala-Asp) box polypeptide 3
218170_at	gb:NM_010048.1 /DEF=Homo sapiens CG1-111 protein (LOC51015), mRNA. /FEA=mRNA /GEN=LOC51015 /PROD=CG1-111 protein /DB_XREF=gi:7705613 / UG=Hs._11085 CG1-111_protein /EI=gb:AE151869.1 qb:NM_016048.1
210293_s_at	gb:BC005032.1 /DEF=Homo sapiens, Sec23 (S. cerevisiae) homolog B, clone MGC:12666, mRNA, complete cds. /FEA=mRNA /PROD=Sec23 (S. cerevisiae)
	homolog B /DB_XREF=gi:13477148 /UG=Hs.173497 Sec23 (S. cerevisiae) homolog B /EI=gb:BC005032.1
221493_at	gb:AU136229.1 /DEF=Homo sapiens mRNA; CDDN DKE2p564d152 (from clone DK7p56d152); complete cds. /FEA=mRNA /GEN=DKF2p56d152 / PROD=hypothetical protein /DB_XREF=gi:12052783 /UG=Hs.278479 TSPY-like /EI=gb:AU136229.1
213306_at	Consensus includes gb:BE865369 /FEA=EST /DB_XREF=gi:11769659 /DB_XREF=est:601659282R1 /CLONE=IMAGE:3895653 /UG=Hs.168102 Human proteinase activated receptor 2 mRNA, 3UTR
201016_at	Consensus includes gb:BE542684 /FEA=EST /DB_XREF=gi:9771329 /DB_XREF=est:601067180F1 /CLONE=IMAGE:3455571 /UG=Hs.4310 eukaryotic translation initiation factor 1A /EI=gb:EC0000793.1 qb:118960.1 qb:NM_001412.1
203411_at	gb:NM_013229.1 /DEF=Homo sapiens monocyte to macrophage differentiation-associated (MMD), mRNA. /FEA=mRNA /GEN=MMD /PROD=monocyte to macrophage differentiated-associated precursor /DB_XREF=gi:6912507 /UG=Hs.79889 monocyte to macrophage differentiation-associated / EI=gb:NM_012329.1

21350_x_at	Consensus includes gb:AW194543 / FEA=EST /DB_XREF=gi:6473381 /DB_XREF=est:xb27c02.x1 /CLONE=IMAGE:2577506 /UG=Hs.234573 Homo sapiens mRNA for rL132
218539_at	gb:NM_017943.1 /DEF=Homo sapiens hypothetical protein FLJ20725 (FLJ20725) , mRNA. /FEA=mRNA /GEN=FLJ20725 /PROD=hypothetical protein FLJ20725 /
	DB_XREF=gi:8923650 /UG=Hs.15467 hypothetical protein FLJ20725 /FL=gb:NM_017943.1
218172_s_at	gb:NM_018630.1 /DEF=Homo sapiens hypothetical protein PRO2577 /PRO2577 /mRNA. /FEA=mRNA /GEN=PRO2577 /PROD=hypothetical protein PRO2577 /
	DB_XREF=gi:8924181 /UG=Hs.241516 hypothetical protein PRO2577 /FL=gb:AF116708.1 gb:NM_018630.1
202538_s_at	gb:NM_0140403.1 /DEF=Homo sapiens DKFZP5401023 protein (DKFZP5401023) , mRNA. /FEA=mRNA /GEN=DKFZP5401023 /PROD=DKFZP5401023 protein /
	DB_XREF=gi:7661633 /UG=Hs.11449 DKFZP5401023 protein /FL=gb:AF151842.1 gb:AL080122.1 gb:NM_014043.1
221504_s_at	gb:AF112204.1 /DEF=Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA, complete cds. /FEA=mRNA /PROD=Vacuolar proton pump subunit SFD alpha isoform /DB_XREF=gi:656195 /UG=Hs.19575 CGI-11 protein /FL=gb:AF298777.1 gb:AF132945.1 gb:AF112204.1 gb:NM_015941.1
212213_x_at	Consensus includes gb:AB011139.1 /DEF=Homo sapiens mRNA for KIAA0567 protein, partial cds. /FEA=mRNA /GEN=KIAA0567 /PROD=KIAA0567 protein /
	DB_XREF=gi:3043657 /UG=Hs.147946 optic atrophy 1 (autosomal dominant)
216652_s_at	Consensus includes gb:AL13767.1 /DEF=Homo sapiens mRNA, cDNA DKFZp434H0872 (from clone DKFZp434H0872) . /FEA=mRNA /DB_XREF=gi:6807841 /UG=Hs.306454 Homo sapiens mRNA, cDNA DKFZp434H0872 (from clone DKFZp434H0872)
221472_at	Consensus includes gb:297033 /DEF=Human DNA sequence from clone RP1-179M20 on chromosome 20 contains a 3 end of a novel gene similar to cellular retinaldehyde-binding protein, the TDE1 gene (Tumour differentially expressed 1), the PKIG gene encoding protein kinase (cAMP-dependent... /FEA=mRNA. 2 /DB_XREF=gi:9650676 /UG=Hs.272168 tumor differentially expressed 1 /FL=gb:AF112227.1 gb:AF153979.1 gb:NM_006811.1
212526_at	Consensus includes gb:AK002207.1 /DEF=Homo sapiens cDNA FLJ11345 fis, clone PLACE1010877, highly similar to Homo sapiens mRNA for KIAA0610 protein. /FEA=mRNA /DB_XREF=gi:7023938 /UG=Hs.118087 KIAA0610 protein
200524_s_at	Consensus includes gb:RA577695 /FEE=EST /DB_XREF=est:nn22102.s1 /CLONE=IMAGE:1081659 /UG=Hs.78825 matrin 3 /FL=gb:NM_018834.1 gb:AB018266.1
201091_s_at	Consensus includes gb:BE748755 /FEE=EST /DB_XREF=gi:10162747 /DB_XREF=est:601571933T1 /CLONE=IMAGE:3838737 /UG=Hs.278554 heterochromatin-like protein 1 /FL=gb:AF136630.1 gb:NM_016587.1
217863_at	Consensus includes gb:AI348378 /FEE=EST /DB_XREF=gi:4085584 /DB_XREF=est:9020h06.x1 /CLONE=IMAGE:1909115 /UG=Hs.75251 DEADH (Asp-Glu-Ala-Asp) box binding protein 1 /FL=gb:AF077951.1 gb:AF167160.1 gb:NM_016166.1
202804_at	Consensus includes gb:AI539710 /FEE=EST /DB_XREF=gi:4453845 /DB_XREF=est:tp77b05.x1 /CLONE=IMAGE:2205297 /UG=Hs.89433 ATP-binding cassette, sub-family C (CFTRRP), member 1 /FL=gb:L05628.1 gb:NM_004996.2
214198_s_at	Consensus includes gb:AU150824 /FEE=EST /DB_XREF=gi:11012345 /DB_XREF=est:AU150824 /CLONE=NT2RP2003689 /UG=Hs.2451 DiGeorge syndrome critical region gene 2
217976_s_at	gb:NM_016141.1 /DEF=Homo sapiens dynein light chain-A (LOC51143) , mRNA. /FEA=mRNA /GEN=LOC51143 /PROD=dynein light chain-A /DB_XREF=gi:7705852 /UG=Hs.266483 dynein light chain-A /FL=gb:AF078849.1 gb:NM_016141.1
202318_s_at	gb:AF306508.1 /DEF=Homo sapiens SUMO-1 specific protease EKS66 mRNA, complete cds. /FEA=mRNA /PROD=SUMO-1 specific protease EKS66 /DB_XREF=gi:11056243 /UG=Hs.27197 SUMO-1-specific protease /FL=gb:AF307849.1 gb:AF306508.1 gb:AF196304.1 gb:NM_015571.1
208673_s_at	gb:AF107405.1 /DEF=Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds. /FEA=mRNA /GEN=SFRS3 /PROD=pre-mRNA splicing factor /DB_XREF=gi:5531903 /UG=Hs.167160 splicing factor, argininoserine-rich 3 /FL=gb:BC0094.1 gb:AF107405.1
218268_at	gb:NM_022771.1 /DEF=Homo sapiens hypothetical protein FLJ12085 (FLJ12085) , mRNA. /FEA=mRNA /GEN=FLJ12085 /PROD=hypothetical protein
	DB_XREF=gi:12232450 /UG=Hs.48827 hypothetical protein FLJ12085 /FL=gb:NM_022771.1
202950_at	gb:BC000961.2 /DEF=Homo sapiens, degenerative spermatocyte (homolog Drosophila; lipid desaturase) /DB_XREF=gi:12803018 /UG=Hs.185973 degenerative spermatoocyte (homolog Drosophila; lipid desaturase) /FL=gb:BC000961.2

218698_at	gb:NM_015957.1 /DEF=Homo sapiens CGI-29 protein (LOC51074), mRNA. /FEA=mRNA /GEN=LOC51074 /PROD=CGI-29 protein /DB_XREF=gi:7705723
	/LOC=Hs_100058
	/FT=gb;AF=132963.1 gb:NM_015957.1
	CGI-29 protein /FT=gb;AF=132963.1 gb:NM_015957.1

Patentansprüche

1. Array bestehend aus Oligo- oder Polynukleotidsonden, die immobilisiert auf einem festen Träger aufgebracht sind, dadurch gekennzeichnet, dass auf der Oberfläche Sequenzen einer Auswahl oder aller der in den Tabellen 1-6 genannten selektiven Monozyten-Makrophagen-Gene gebunden sind.
5
- 10 2. Array nach Anspruch 1, dadurch gekennzeichnet, dass gegebenenfalls zusätzlich weitere Gene verwendet werden, von denen bekannt ist, dass sie in jeder Zelle exprimiert werden und zur Grundausstattung einer Zelle gehören.
- 15 3. Array nach Anspruch 1 und 2, dadurch gekennzeichnet, dass mit den genannten Genen komplementäre RNA auf der Oberfläche des Arrays gebunden ist zum inversen Nachweis über die in den Tabellen 1-6 dargestellten Gene oder Gensequenzen.
20
- 25 4. Array nach Anspruch 1 bis 3, dadurch gekennzeichnet, dass die Gene, deren Teil- und Oligomersequenzen krankheits- und nebenwirkungsrelevante selektionierte Gene der rheumatoiden Arthritis oder anderer chronisch entzündlichen Erkrankungen vor und nach anti-TNF-Therapie sind.
- 30 5. Array nach Anspruch 1 bis 4, dadurch gekennzeichnet, dass die Gene, deren Teilesequenzen und Oligomersequenzen krankheitsspezifisch regulierte Gene des Monozyten/Makrophagen-Zellsystems sind.

6. Array nach Anspruch 1 bis 5, dadurch gekennzeichnet, dass auf der Oberfläche gegebenenfalls auch Allele, Derivate und/oder Splicingvarianten der Gen- bzw. Genteilsequenzen und Oligomersequenzen vorliegen.

5

7. Array nach Anspruch 1 bis 6, dadurch gekennzeichnet, dass es auf der Oberfläche Gensequenzen enthält, die mindestens eine Teil-Sequenzidentität von 80 % in den Protein-kodierenden Abschnitten der mRNA besitzen.

10

8. Array nach Anspruch 1 bis 7, dadurch gekennzeichnet, dass die Oberfläche der Träger mit reaktiven Gruppen, Metallverbindungen oder Legierungen beschichtet ist.

15

9. Array nach Anspruch 1 bis 8, dadurch gekennzeichnet, dass die Gene oder Gensequenzen durch Spottingverfahren von cDNA, Immobilisierungs-verfahren und Syntheseeverfahren von Oligomeren oder spiegelbildlich in Form von RNA aufgebracht sind.

20

10. Verwendung des Arrays nach Anspruch 1 bis 9 mit Proben, die zum Nachweis Fluoreszenzfarbstoff-, Enzym-, Protein- oder radioaktiv markiert sind und eine Verstärkung zulassen.

25

11. Verwendung des Arrays nach Anspruch 1 bis 9 mit Proben, dadurch gekennzeichnet, dass die Verstärkung der Signale über gekoppelte alkalische Phosphatase, Peroxidase, Biotin Digoxigenin-, Proteinmoleküle, (Edel-)Metallchelate oder Beads erfolgt.

30

12. Verwendung des Arrays nach Anspruch 1 bis 9 mit Proben, dadurch gekennzeichnet, dass zur zusätzlichen Verstärkung der Signale Streptavidin, (Edel-)Metallchelate, Beads oder Antikörper eingesetzt werden.

5

13. Verwendung des Arrays nach Anspruch 1 bis 9 zum inversen Nachweis festphasengebundener Total-RNA oder messenger-RNA.

10 14. Verwendung des Arrays nach Anspruch 1 bis 9 zur Messung der Monozyten/Makrophagen-Aktivierung oder der Entzündungsaktivität im Blut oder im Zellgewebe.

15 15. Verwendung des Arrays nach Anspruch 1 bis 9 zur Feindiagnostik sowie zur Früherkennung von entzündlichen Erkrankungen und der rheumatoïden Arthritis.

20 16. Verwendung des Arrays nach Anspruch 1 bis 9 zur Verfolgung von Nebenwirkungen bei der anti-TNF-Therapie von entzündlichen Erkrankungen und der rheumatoïden Arthritis.

25 17. Verwendung des Arrays nach Anspruch 1 bis 9 zur Überwachung der Therapie und Erstellung einer Prognose bei entzündlichen Erkrankungen und der rheumatoïden Arthritis.

30 18. Verwendung der Arrays nach Anspruch 1 bis 9 zur Identifizierung von pharmazeutischen Targets bei entzündlichen Erkrankungen und der rheumatoïden Arthritis.

19. Verwendung der Gene oder Gensequenzen nach Tabelle 1-6 zu Einzelgennachweisverfahren, vorzugsweise reverse Transkriptions-PCR (RT-PCR) .

5 20. Verwendung der Gene oder Gensequenzen nach Tabelle 1-6, dadurch gekennzeichnet, dass sie mit einer Markierung oder einer Reporterfunktion ausgestattet sind.

10 21. Verwendung der Gene oder Gensequenzen nach Tabelle 1-6 zum reversen Nachweis festphasengebundener Total-RNA oder messenger-RNA in einem RNA-Array mit bis zu 500 Gewebs- und/oder Blutproben.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/DE 03/01822

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHEDMinimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, EMBASE, Sequence Search**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>STUHLMÜLLER ET AL.: "Identification of known and novel genes in activated monocytes from patients with rheumatoid arthritis" ARTHRITIS & RHEUMATISM, vol. 43, no. 4, April 2000 (2000-04), pages 775-790, XP002255228 the whole document</p> <p>-----</p> <p>HELLER R A ET AL: "Discovery and analysis of inflammatory disease-related genes using cDNA microarrays" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, US, no. 94, pages 2150-2155, XP002076789 ISSN: 0027-8424 the whole document</p> <p>-----</p>	
A		-/-

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

° Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

23 September 2003

Date of mailing of the international search report

27.01.2004

Name and mailing address of the ISA

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Authorized officer

Bort, S

INTERNATIONAL SEARCH REPORT

International Application No

PCT/DE 03/01822

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SMEETS ET AL.: "Quantitative analysis of chemokine expression in rheumatoid synovial tissue after treatment with anti-TNF and IFN-beta" ARTHRITIS AND RHEUMATISM, vol. 42, no. 9, September 1999 (1999-09), page s93, XP008022391 abstract -----	
A	DATABASE EBI [Online] 7 January 1995 (1995-01-07), TRUCCO: "Human MHC clas II DG-beta associated with DRw6, DQw1 protein, complete cds." XP002255230 Database accession no. M17565 -----	

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DE 03/01822**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See continuation sheet

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

1-21 (all in part)

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

OTHER INFORMATION	PCT/ISA/ 210
The International Searching Authority has determined that this international application contains multiple (groups of) inventions, namely	
1. Claims 1-21 (all in part)	
Inventions 1-1500	
<p>array consisting of at least one of the genes specified in tables 1-6, and use of the array,</p> <p>where the gene bank accession numbers corresponding to gene sequence are:</p> <ul style="list-style-type: none">- for Invention 1: M17565.1- for Invention 2: X00452.1- for Inventions 3-1500: BF338947-NM_015957.1 <p>---</p>	

INTERNATIONALER RECHERCHENBERICHT

Internationales Aktenzeichen

DE 03/01822

A. KLASIFIZIERUNG DES ANMELDUNGSGEGENSTANDES
IPK 7 C12Q1/68

Nach der Internationalen Patentklassifikation (IPK) oder nach der nationalen Klassifikation und der IPK

B. RECHERCHIERTE GEBIETE

Recherchierte Mindestprüfstoff (Klassifikationssystem und Klassifikationssymbole)
IPK 7 C12Q

Recherchierte aber nicht zum Mindestprüfstoff gehörende Veröffentlichungen, soweit diese unter die recherchierten Gebiete fallen

Während der Internationalen Recherche konsultierte elektronische Datenbank (Name der Datenbank und evtl. verwendete Suchbegriffe)

EPO-Internal, BIOSIS, EMBASE, Sequence Search

C. ALS WESENTLICH ANGESEHENE UNTERLAGEN

Kategorie°	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
A	STUHLMÜLLER ET AL.: "Identification of known and novel genes in activated monocytes from patients with rheumatoid arthritis" ARTHRITIS & RHEUMATISM, Bd. 43, Nr. 4, April 2000 (2000-04), Seiten 775-790, XP002255228 das ganze Dokument -----	
A	HELLER R A ET AL: "Discovery and analysis of inflammatory disease-related genes using cDNA microarrays" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, US, Nr. 94, Seiten 2150-2155, XP002076789 ISSN: 0027-8424 das ganze Dokument -----	
	-/-	

 Weitere Veröffentlichungen sind der Fortsetzung von Feld C zu entnehmen Siehe Anhang Patentfamilie

- ° Besondere Kategorien von angegebenen Veröffentlichungen :
 - "A" Veröffentlichung, die den allgemeinen Stand der Technik definiert, aber nicht als besonders bedeutsam anzusehen ist
 - "E" älteres Dokument, das jedoch erst am oder nach dem internationalen Anmeldedatum veröffentlicht worden ist
 - "L" Veröffentlichung, die geeignet ist, einen Prioritätsanspruch zweifelhaft erscheinen zu lassen, oder durch die das Veröffentlichungsdatum einer anderen im Recherchenbericht genannten Veröffentlichung belegt werden soll oder die aus einem anderen besonderen Grund angegeben ist (wie ausgeführt)
 - "O" Veröffentlichung, die sich auf eine mündliche Offenbarung, eine Benutzung, eine Ausstellung oder andere Maßnahmen bezieht
 - "P" Veröffentlichung, die vor dem internationalen Anmeldedatum, aber nach dem beanspruchten Prioritätsdatum veröffentlicht worden ist
- "T" Spätere Veröffentlichung, die nach dem internationalen Anmeldedatum oder dem Prioritätsdatum veröffentlicht worden ist und mit der Anmeldung nicht kollidiert, sondern nur zum Verständnis des der Erfindung zugrundeliegenden Prinzips oder der ihr zugrundeliegenden Theorie angegeben ist
- "X" Veröffentlichung von besonderer Bedeutung; die beanspruchte Erfindung kann allein aufgrund dieser Veröffentlichung nicht als neu oder auf erfinderischer Tätigkeit beruhend betrachtet werden
- "Y" Veröffentlichung von besonderer Bedeutung; die beanspruchte Erfindung kann nicht als auf erfinderischer Tätigkeit beruhend betrachtet werden, wenn die Veröffentlichung mit einer oder mehreren anderen Veröffentlichungen dieser Kategorie in Verbindung gebracht wird und diese Verbindung für einen Fachmann naheliegend ist
- "&" Veröffentlichung, die Mitglied derselben Patentfamilie ist

Datum des Abschlusses der internationalen Recherche 23. September 2003	Absendedatum des internationalen Recherchenberichts 27.01.2004
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Name und Postanschrift der Internationalen Recherchenbehörde
Europäisches Patentamt, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Bevollmächtigter Bediensteter

Bort, S

INTERNATIONALER RECHERCHENBERICHT

Internationales Aktenzeichen

/DE 03/01822

C.(Fortsetzung) ALS WESENTLICH ANGESEHENE UNTERLAGEN

Kategorie*	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
A	<p>SMEETS ET AL.: "Quantitative analysis of chemokine expression in rheumatoid synovial tissue after treatment with anti-TNF and IFN-beta" ARTHRITIS AND RHEUMATISM, Bd. 42, Nr. 9, September 1999 (1999-09), Seite s93, XP008022391 Zusammenfassung</p> <p>-----</p> <p>DATABASE EBI [Online] 7. Januar 1995 (1995-01-07), TRUCCO: "Human MHC clas II DG-beta associated with DRw6, DQw1 protein, complete cds." XP002255230 Database accession no. M17565</p> <p>-----</p>	
A		

Feld I Bemerkungen zu den Ansprüchen, die sich als nicht recherchierbar erwiesen haben (Fortsetzung von Punkt 2 auf Blatt 1)

Gemäß Artikel 17(2)a) wurde aus folgenden Gründen für bestimmte Ansprüche kein Recherchenbericht erstellt:

1. Ansprüche Nr.
weil sie sich auf Gegenstände beziehen, zu deren Recherche die Behörde nicht verpflichtet ist, nämlich

2. Ansprüche Nr.
weil sie sich auf Teile der internationalen Anmeldung beziehen, die den vorgeschriebenen Anforderungen so wenig entsprechen, daß eine sinnvolle internationale Recherche nicht durchgeführt werden kann, nämlich

3. Ansprüche Nr.
weil es sich dabei um abhängige Ansprüche handelt, die nicht entsprechend Satz 2 und 3 der Regel 6.4 a) abgefaßt sind.

Feld II Bemerkungen bei mangelnder Einheitlichkeit der Erfindung (Fortsetzung von Punkt 3 auf Blatt 1)

Die internationale Recherchenbehörde hat festgestellt, daß diese internationale Anmeldung mehrere Erfindungen enthält:

siehe Zusatzblatt

1. Da der Anmelder alle erforderlichen zusätzlichen Recherchengebühren rechtzeitig entrichtet hat, erstreckt sich dieser internationale Recherchenbericht auf alle recherchierbaren Ansprüche.

2. Da für alle recherchierbaren Ansprüche die Recherche ohne einen Arbeitsaufwand durchgeführt werden konnte, der eine zusätzliche Recherchengebühr gerechtfertigt hätte, hat die Behörde nicht zur Zahlung einer solchen Gebühr aufgefordert.

3. Da der Anmelder nur einige der erforderlichen zusätzlichen Recherchengebühren rechtzeitig entrichtet hat, erstreckt sich dieser internationale Recherchenbericht nur auf die Ansprüche, für die Gebühren entrichtet worden sind, nämlich auf die Ansprüche Nr.

4. Der Anmelder hat die erforderlichen zusätzlichen Recherchengebühren nicht rechtzeitig entrichtet. Der internationale Recherchenbericht beschränkt sich daher auf die in den Ansprüchen zuerst erwähnte Erfindung; diese ist in folgenden Ansprüchen erfaßt:
1-21 (alle teilweise)

Bemerkungen hinsichtlich eines Widerspruchs

- Die zusätzlichen Gebühren wurden vom Anmelder unter Widerspruch gezahlt.
 Die Zahlung zusätzlicher Recherchengebühren erfolgte ohne Widerspruch.

WEITERE ANGABEN

PCT/ISA/ 210

Die internationale Recherchenbehörde hat festgestellt, dass diese internationale Anmeldung mehrere (Gruppen von) Erfindungen enthält, nämlich:

1. Ansprüche: 1-21 (alle teilweise)

Erfindungen 1-1500

Array bestehend aus mindesten eines der in Tabellen 1-6 aufgeführten Gene; und verwendung des Arrays,

wo die Sequenz des Gens entsprechendes Genebank accession no. ist:

- für Erfindung 1: M17565.1
- für Erfindung 2: X00452.1
- für Erfindungen 3-1500: BF338947-NM_015957.1
-